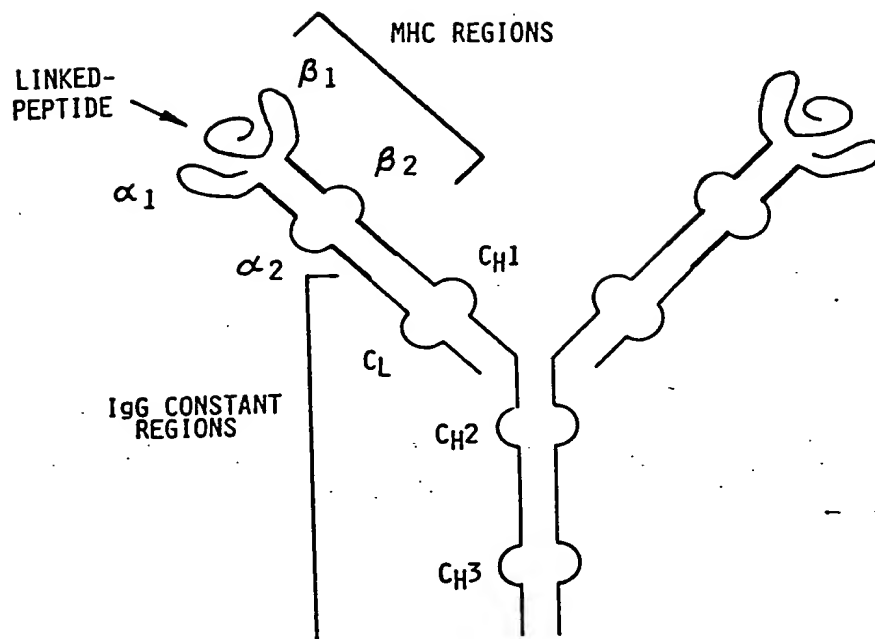


**FIG. 1B**



**FIG. 1C**

004164-050301

TOTAL RNA ISOLATED  
FROM A20 CELLS

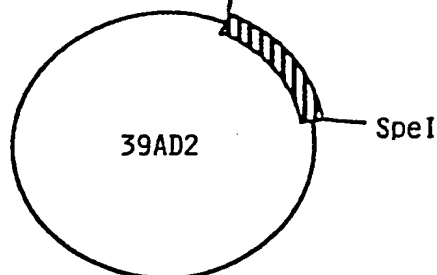
↓  
SYNTHESIS OF FIRST STRAND cDNA USING  
OPR101 OLIGONUCLEOTIDE PRIMER

I-A<sup>d</sup> αCHAIN  
SPECIFIC cDNA

↓  
PCR AMPLIFICATION WITH  
OPR101 & OPR100 PRIMERS

NcoI SpeI  
α1-α2 PCR  
PRODUCT

NcoI/SpeI  
DIGEST

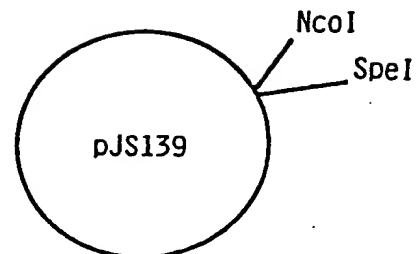
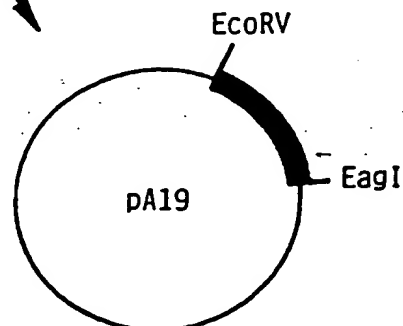


TEMPLATE FOR PCR  
AMPLIFICATIONS

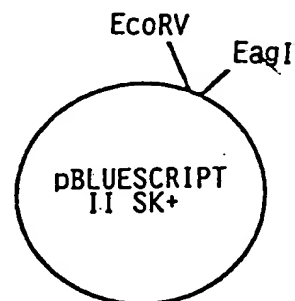
↓  
PCR WITH OPR107  
& OPR108 PRIMERS

EcoRV EagI  
α1-α2 PCR  
PRODUCT

EcoRV/EagI  
DIGEST



NcoI/SpeI  
DIGEST



EcoRV/EagI DIGEST

FIG. 2

TOTAL RNA ISOLATED  
FROM A20 CELLS

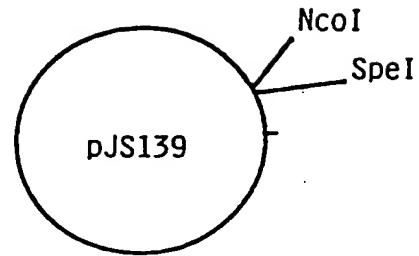
↓  
SYNTHESIS OF FIRST STRAND cDNA USING  
OLIGO dT PRIMER

cDNA TEMPLATE

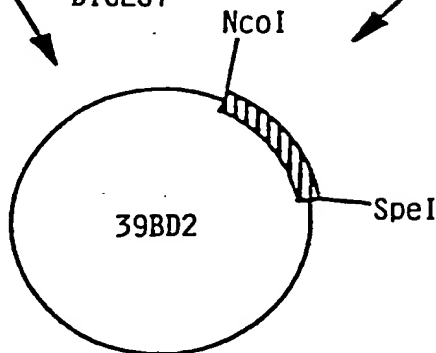
↓  
PCR AMPLIFICATION WITH  
OPR102 & OPR104 PRIMERS

NcoI SpeI  
β1-β2 PCR  
PRODUCT

NcoI/SpeI  
DIGEST



NcoI/SpeI  
DIGEST

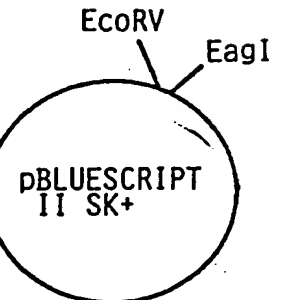
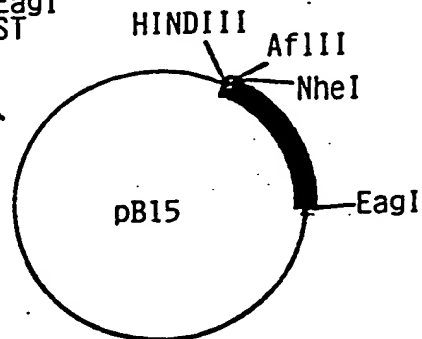


TEMPLATE FOR PCR  
AMPLIFICATIONS

↓  
PCR WITH OPR106  
& OPR112 PRIMERS

EcoRV EagI  
NheI  
AflIII  
Linker-β1-β2  
PCR PRODUCT

EcoRV/EagI  
DIGEST



EcoRV EagI  
DIGEST

FIG. 3A

MUTATION IN LINKER REGION-  
NO EcoRV SITE PRESENT

0948164-05031  
10E050-49T84860

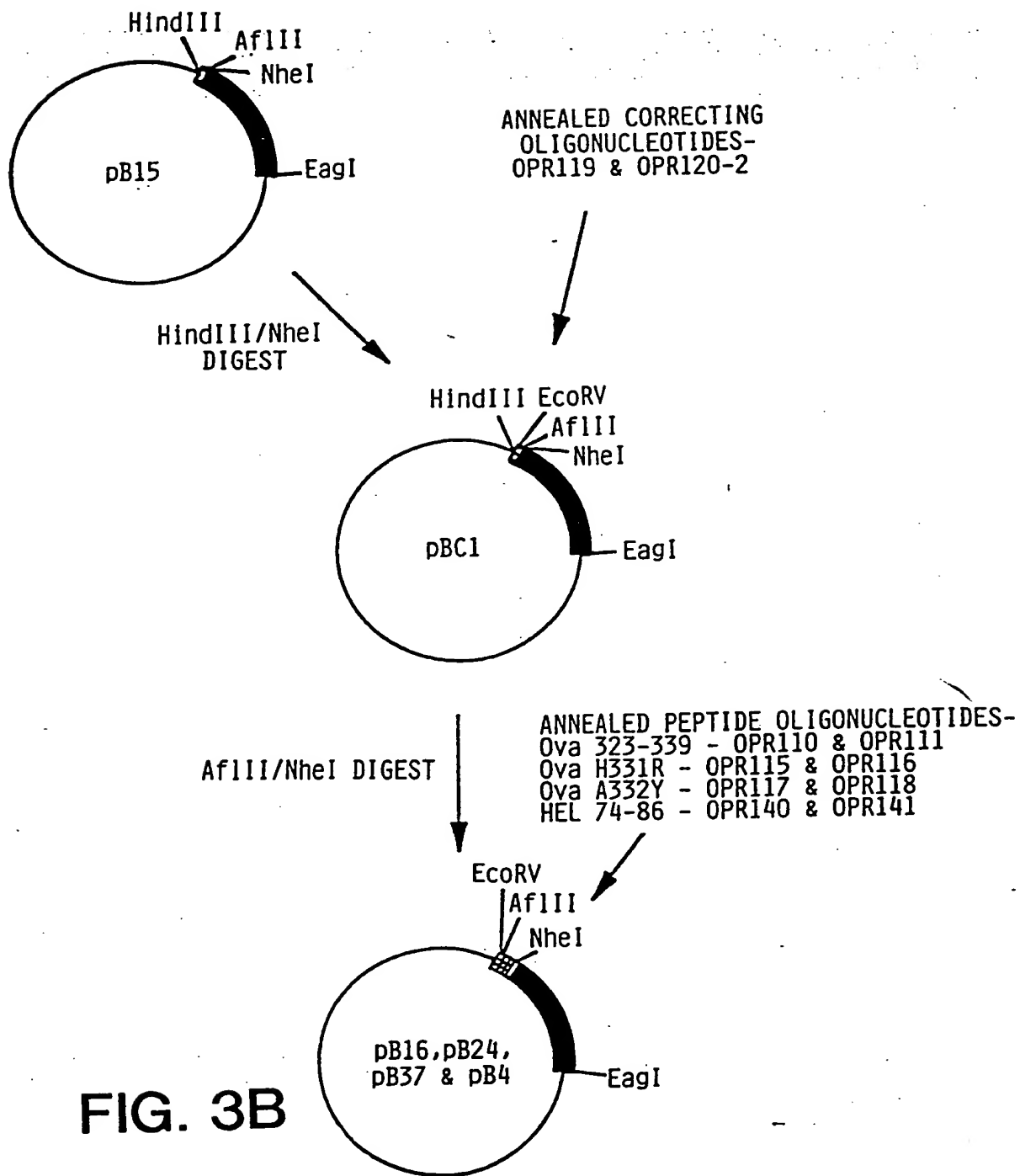
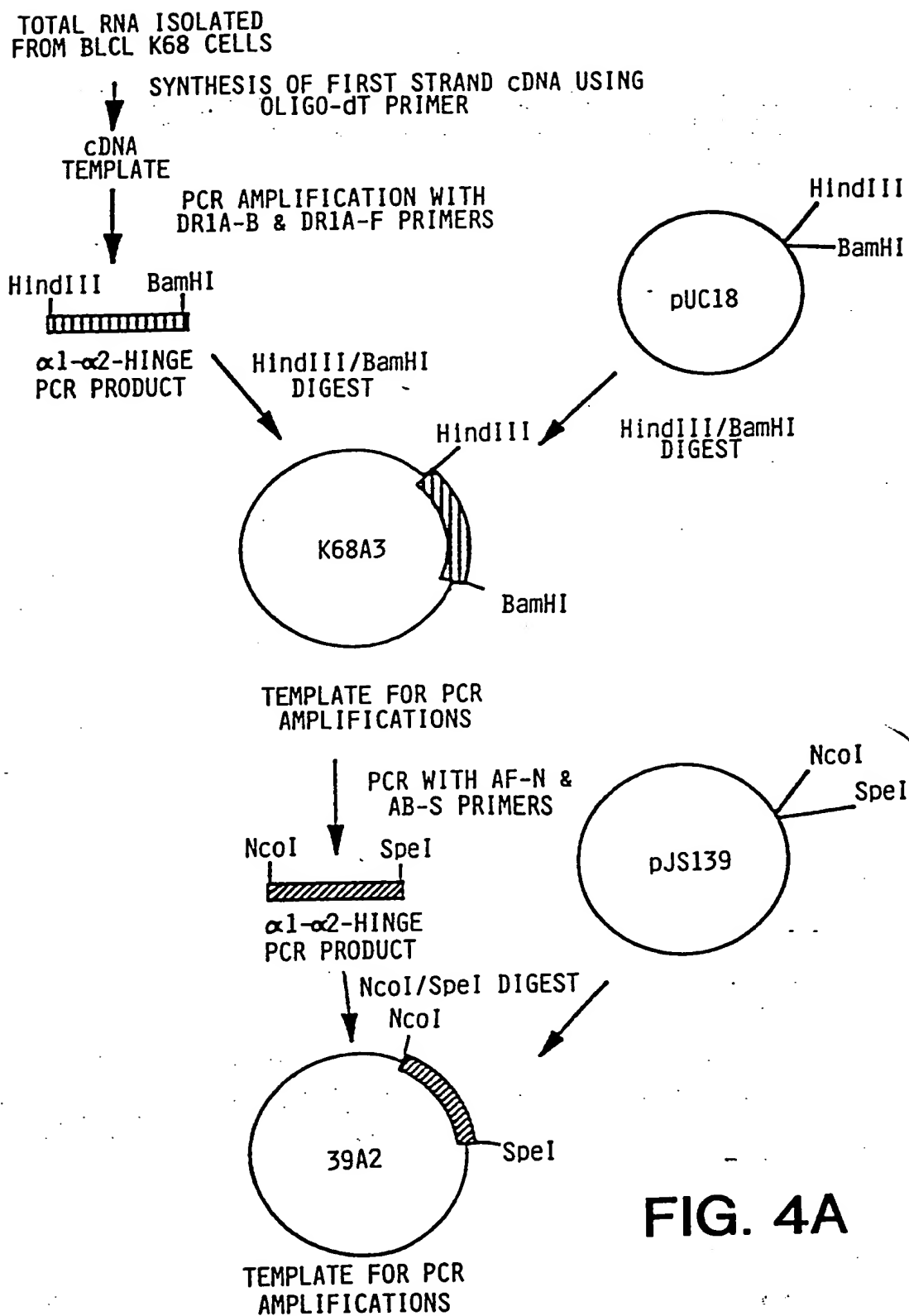
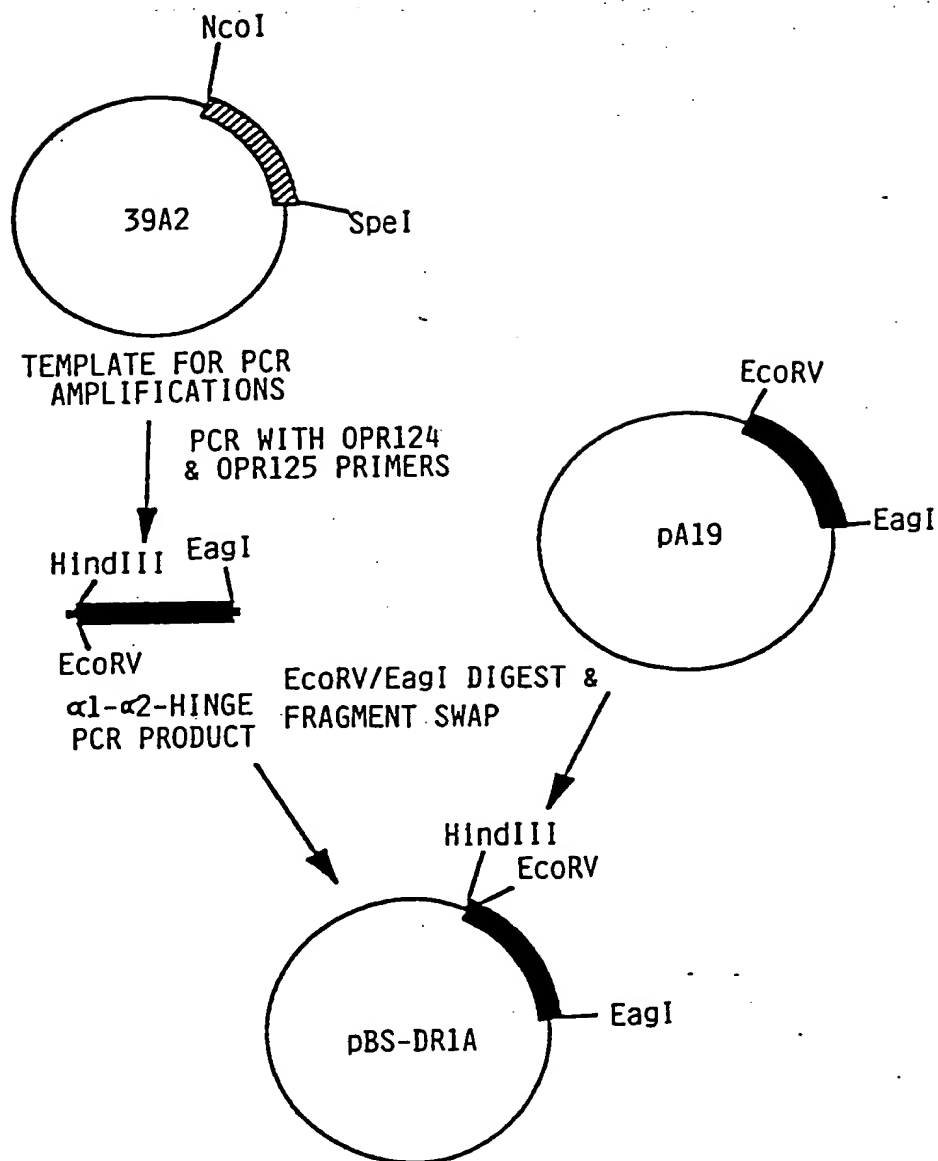


FIG. 3B

TOE050"49T84260



**FIG. 4B**

T0E050"49T87360

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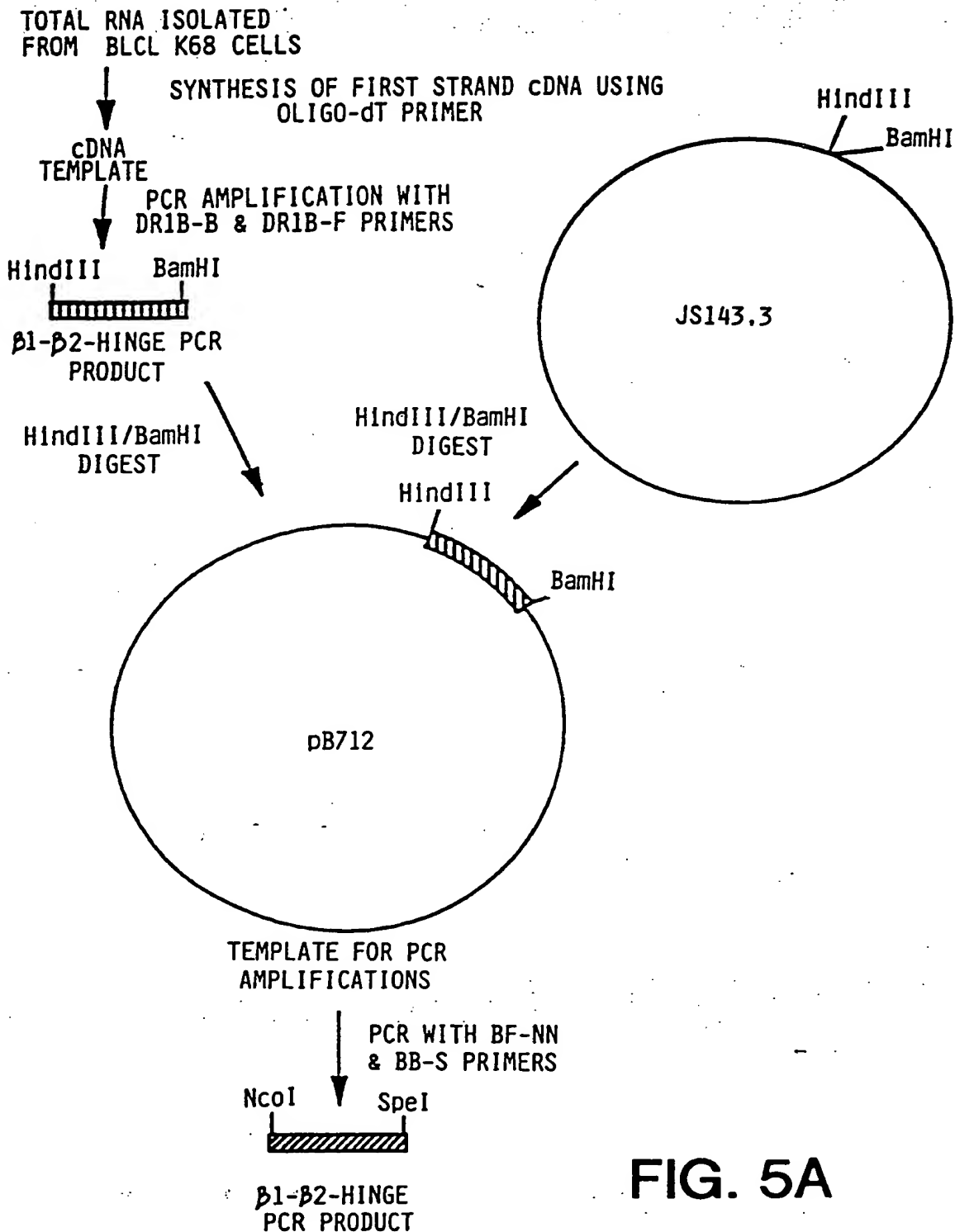


FIG. 5A

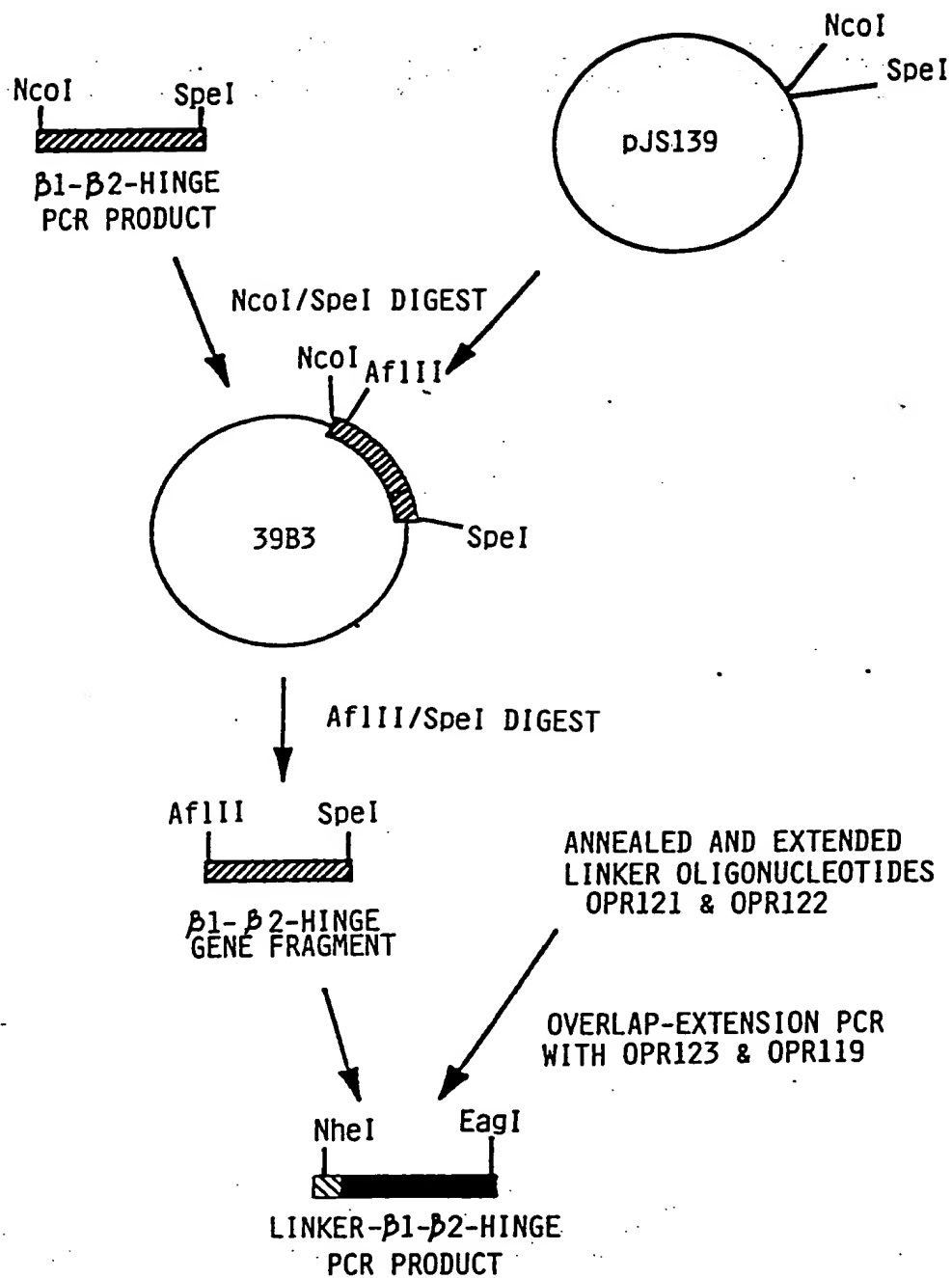


FIG. 5B

094454-0500



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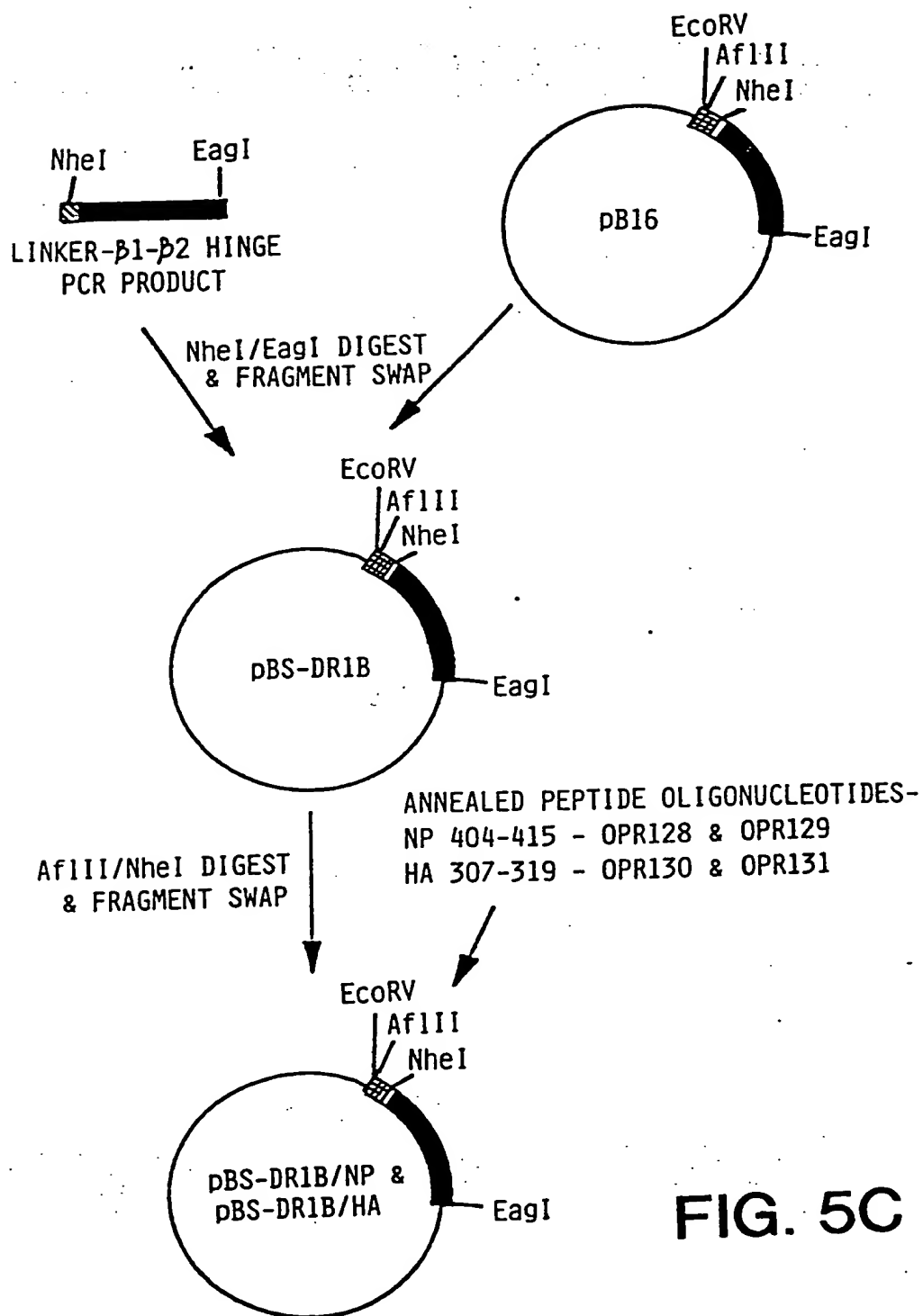


FIG. 5C

09848154-050301

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TOTAL RNA ISOLATED FROM  
SJL MOUSE SPLEEN CELLS

↓  
SYNTHESIS OF FIRST STRAND cDNA USING  
OPR101 OLIGONUCLEOTIDE PRIMER

I-A S  $\alpha$ CHAIN  
SPECIFIC cDNA

↓  
PCR AMPLIFICATION WITH  
OPR100 & OPR101 PRIMERS

NcoI SpeI  
α1-α2PCR  
PRODUCT

↓  
PCR AMPLIFICATION WITH  
OPR107 & OPR108 PRIMERS

EcoRV EagI  
α1-α2 PCR  
PRODUCT

EcoRV/EagI DIGEST  
& FRAGMENT SWAP

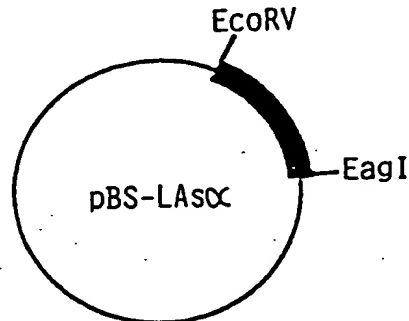
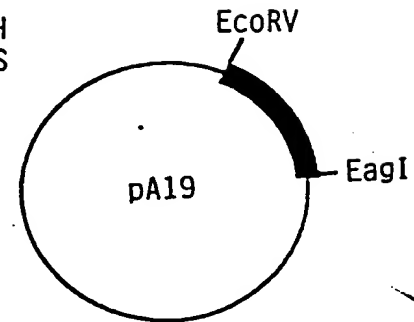


FIG. 6

09646164-050301  
T0E050-49T84360

TOTAL RNA ISOLATED FROM  
SJL MOUSE SPLEEN CELLS

SYNTHESIS OF FIRST STRAND cDNA USING  
OPR106 PRIMER

I-A<sup>S</sup>  $\beta$  SPECIFIC  
cDNA TEMPLATE

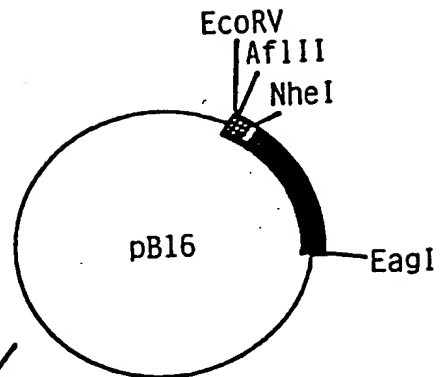
PCR AMPLIFICATION WITH  
VW310 & OPR106 PRIMERS

$\beta$ 1- $\beta$ 2 PCR PRODUCT

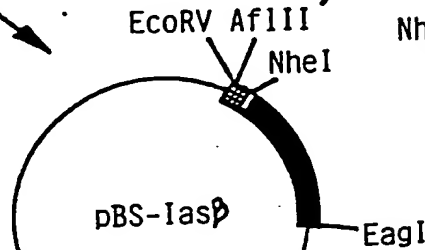
PCR AMPLIFICATION WITH  
VW309 & OPR106 PRIMERS

NheI EagI  
LINKER- $\beta$ 1- $\beta$ 2  
PCR PRODUCT

NheI/EagI DIGEST &  
FRAGMENT SWAP



NheI/EagI  
DIGEST



ANNEALED PEPTIDE OLIGONUCLEOTIDES-  
MBP 91-103 - VW315 & VW316  
PLP 139-151 - VW313 & VW314  
MBP 1-14 - VW317 & VW318

AfIII/NheI DIGEST  
& FRAGMENT SWAP

EcoRV  
AfIII  
NheI

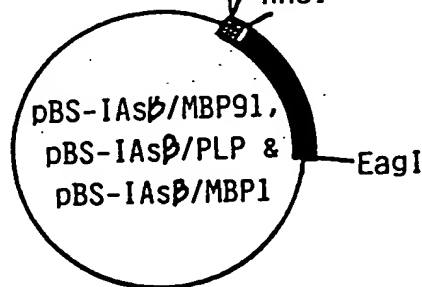


FIG. 7

050301 "4918164" 050301

I-Ad/I-As PCR PRIMERS AND CLONING OLIGONUCLEOTIDES 12 / 69  
(RESTRICTION SITE ARE UNDERLINED).

OPR100  
5'-GGG GGG GCC ATG GCC GAA GAC GAC GAC ATT GAG GCC GAC-3'

OPR101  
5'-GCG GCG ACT AGT CCA GTG TTT CAG AAC CGG CTC-3'

OPR107  
5'-CCC CCC GAT ATC TCA GCT TCC AGC AGT GGA GAC GAC ATT GAG  
GCC G-3'

OPR108  
5'-CCC CCC CGG CCG CTA CTT ACG TTT CCA GTG TTT CAG AAC CGG  
C-3'

OPR102  
5'-GGG GGG GCC ATG GCC GGA AAC TCC GAA AGG CAT TTC G-3'

OPR104  
5'-GCG GCG ACT AGT CCA CTC CAC AGT GAT GGG GC-3'

OPR106  
5'-CCC CCC CGG CCG TAC CTG AGG ACC ACT CCA CAG TGA TGG-3'

OPR112  
5'-CCC CCC GAT ATC ACA GGT GTC TTA AGT GCT AGC GGA GGG GGC  
GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC-3'

OPR119  
5'-AGC ITG ATA TCA CAG GTG TCT TAA GTG GAG-3'.

OPR120-2  
5'-CTA GCT CCA CTT AAG ACA CCT GTG ATA TCA-3'

VW310  
5'-TCC GGA GGC GGC GGA GAC TCC GAA AGG CAT TTC G-3'

VW309  
5'-CGA TCG CTA GCG GCG GTG GTG GTT CCG GTG GCG GCG GAG-3'

OPR136  
5'-CCC CCC AGG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC  
TG-3'

OPR139  
5'-CCC CCC GAG CTC GAA TTC TCA TAA AGG CCC TGG GTG TCT G-3'

OPR132  
5'-CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA  
GC-3'

OPR133  
5'-CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'

OPR134  
5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135  
5'-CCC CCC GAG CTC GAA TTC TCA CTG CAG GAG CCC TGC TGG-3'

FIG. 8A

0948164-050301

## HLA-DRI PCR PRIMERS AND CLONING OLIGONUCLEOTIDES.

DRIA-F  
5'-GGG GGG AAG CTT ATG ATC AAA GAA GAA CAT GTG ATC ATC-3'

DRIA-B  
5'-GCG GCG GGA TCC GTT CTC TGT AGT CTC TGG GAG AGG-3'

DRIB-F  
5'-GGG GGG AAG CTT ATG GGG GAC ACC CGA CCA CGT TTC TTG TGG  
CAG C-3'

AF-N  
5'-GGG GGG GCC ATG GCC ATC AAA GAA GAA CAT GTG ATC ATC-3'

AB-S  
5'-GCG GCG ACT AGT GTT CTC TGT AGT CTC TGG GAG AGG-3'

OPR124  
5'-GGG GGG AAG CTT GAT ATC TCA GCT TCC AGC AGT AGT ATC AAA  
GAA GAA CAT GTG ATC-3'

OPR125  
5'-GGG GGG CGG CCG CTA CTT ACG TTT CTC TGG GAG AGG GCT TGG  
AGC-3'

DRIB-B  
5'-GCG GCG GGA TCC CTT GCT CTG TGC AGA TTC AGA CC-3'

BF-NN  
5'-GGG GGG GCC ATG GCC GGA TCC GCT AGC GGG GAC ACC CGA CCA  
CGT TTC TTG-3'

BB-S  
5'-GCG GCG ACT AGT CTT GCT CTG TGC AGA TTC AGA CCG-3'

OPR121  
5'-GTT GTC TTA AGT GGA GCT AGC GGA GGG GGC GGG TCC GGA GGT  
GGT GGG GAC ACC CG-3'

OPR122  
5'-GAA ATG ACA TTC AAA CTT CAG CTG CCA CAA GAA ACG TGG TCG  
GGT GTC CCC ACC ACC-3'

OPR123  
5'-GGG GGG CGG CCG TAC CTG AGG ACT TGC TCT GTG CAG ATT CAG-  
3'

FIG. 8B

09843164-050301

## PEPTIDE OLIGONUCLEOTIDES.

Ova 323-339

OPR110

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC GCT GAA ATC  
AAC GAA GCT GGT CGT G-3'

OPR111

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC TGA GCA GCG TGA  
ACA GCC TGA GAG ATA C-3'

Ova H331R

OPR115

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CGG GCT GAA ATC  
AAC GAA GCT GGT CGT G-3'

OPR116

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC CGA GCA GCG TGA  
ACA GCC TGA GAG ATA C-3'

Ova A332Y

OPR117

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC TAC GAA ATC  
AAC GAA GCT GGT CGT G-3'

OPR116

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA TAG TGA GCA GCG TGA  
ACA GCC TGA GAG ATA C-3'

HEL 74-86

OPR140

5'-TTA AGT AAC CTG TGC AAC ATC CCC TGC AGC GCC CTG CTG AGC  
TCC G-3'

OPR141

5'-CTA GCG GAG CTC AGC AGG GCG CTG CAG GGG ATG TTG CAC AGG  
TTA C-3'

NP 404-415

OPR128

5'-TTA AGT CAG ATC AGC GTG CAG CCC GCC TTC AGC GTG CAG G-3'

FIG. 8C

10050-1978-1360

OPR129  
5'-CTA GCC TGC ACG CTG AAG GCG GGC TGA ACG CTG ATC TGA C-3'

HA 307-319

OPR130  
5'-TTA AGT CCC AAG TAC GTG AAG CAG AAC ACC CTG AAG CTG GCC  
ACC G-3'

OPR131  
5'-CTA GCG GTG GCC AGC TTC AGG GTG TTC TGC TTC ACG TAC TTG  
GGA C-3'

MBP 91-103

VW315  
5'-TTA AGT CAC TAT GGC TCC CTG CCG CAG AAG TCC CAG CAC GGG  
CGC G-3'

VW316  
5'-CTA GCG CGC CCG TGC TGG GAC TTC TGC GGC AGG GAG CCA TAG  
TGA C-3'

PLP 139-151

VW313  
5'-TTA CAT CAC TCC CTG GGC AAG TGG CTG GGC CAC CCG GAC AAG  
TTC G-3'

VW314  
5'-CTA GCG AAC TTG TTC GGG TGG CCC AGC CAC TTG CCC AGG GAG  
TGA C-3'

MBP 1-14

VW317  
5'-TTA AGT ATG GCA TCC CAG AAG CGC CCG TCC CAG CGC TCC AAG  
TAC CTG G-3'

VW316  
5'-CTA GCC AGG TAC TTG GAG CGC TGG GAC GGG CGC TTC TGG GAT  
GCC ATA C-3'

FIG. 8D

09043164-050301

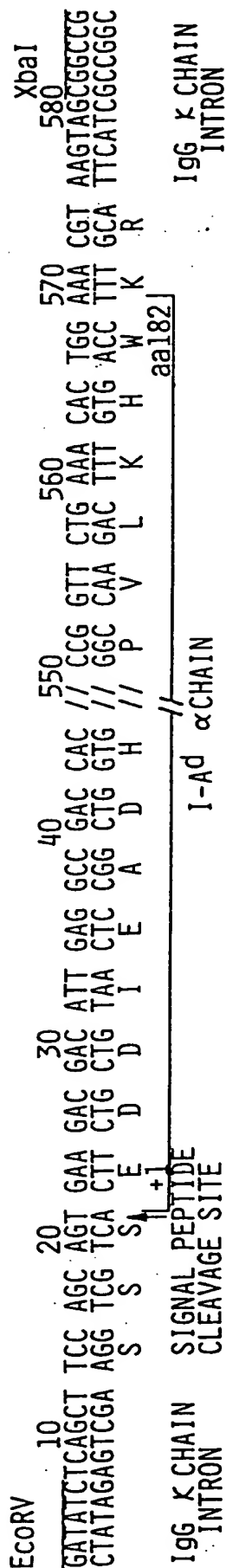
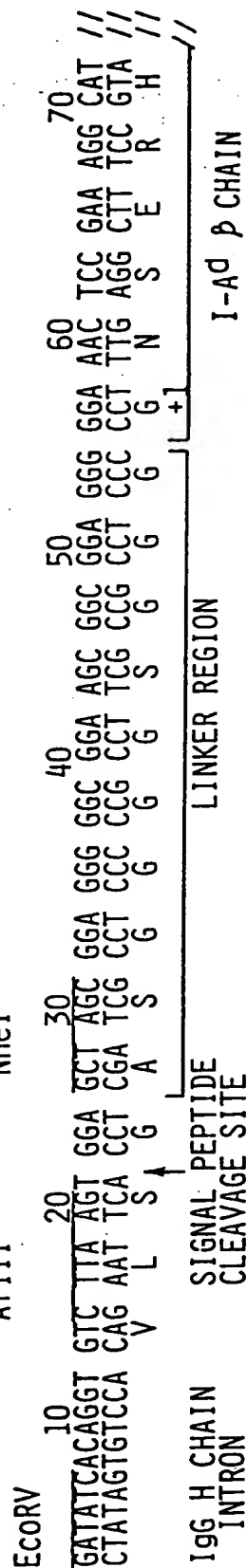


FIG. 9A

RESTRICTION SITES FOR INSERTION OF OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST



XbaI

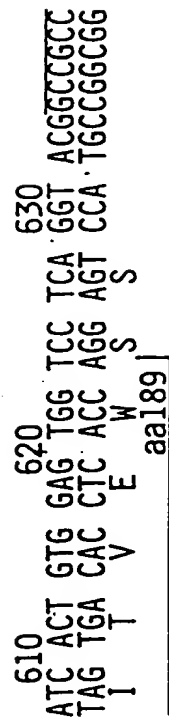
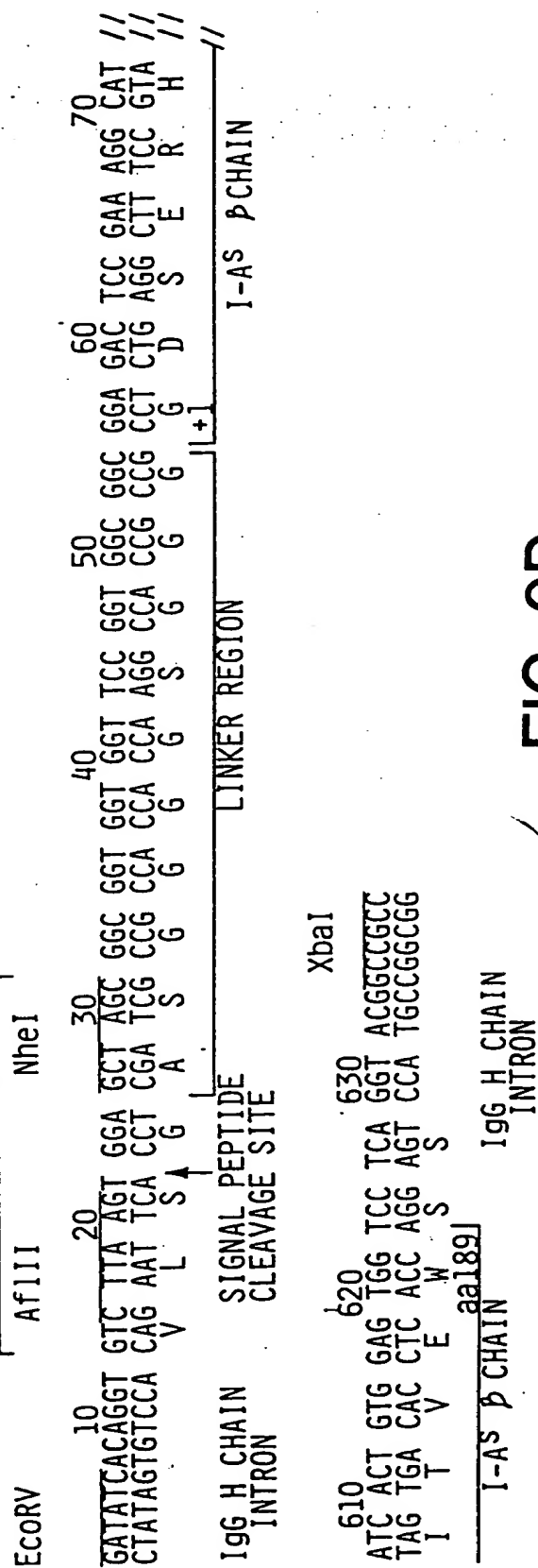
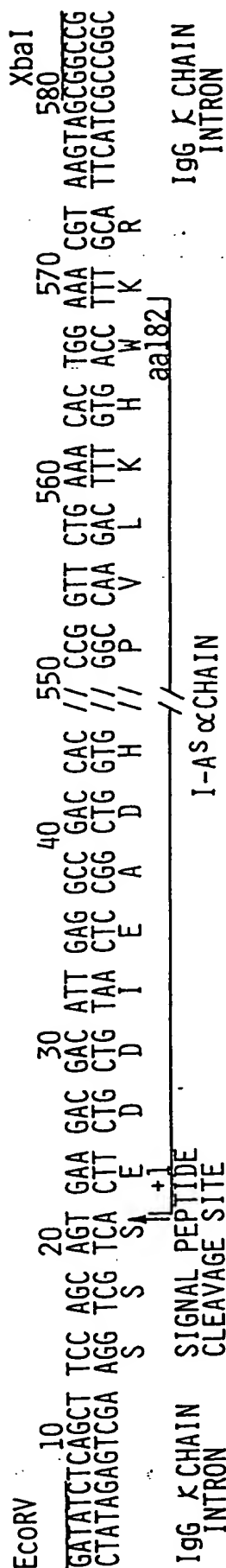
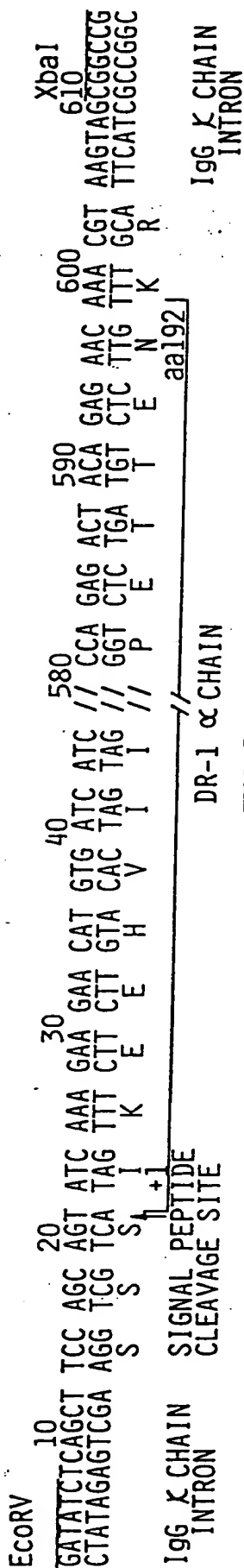


FIG. 9B

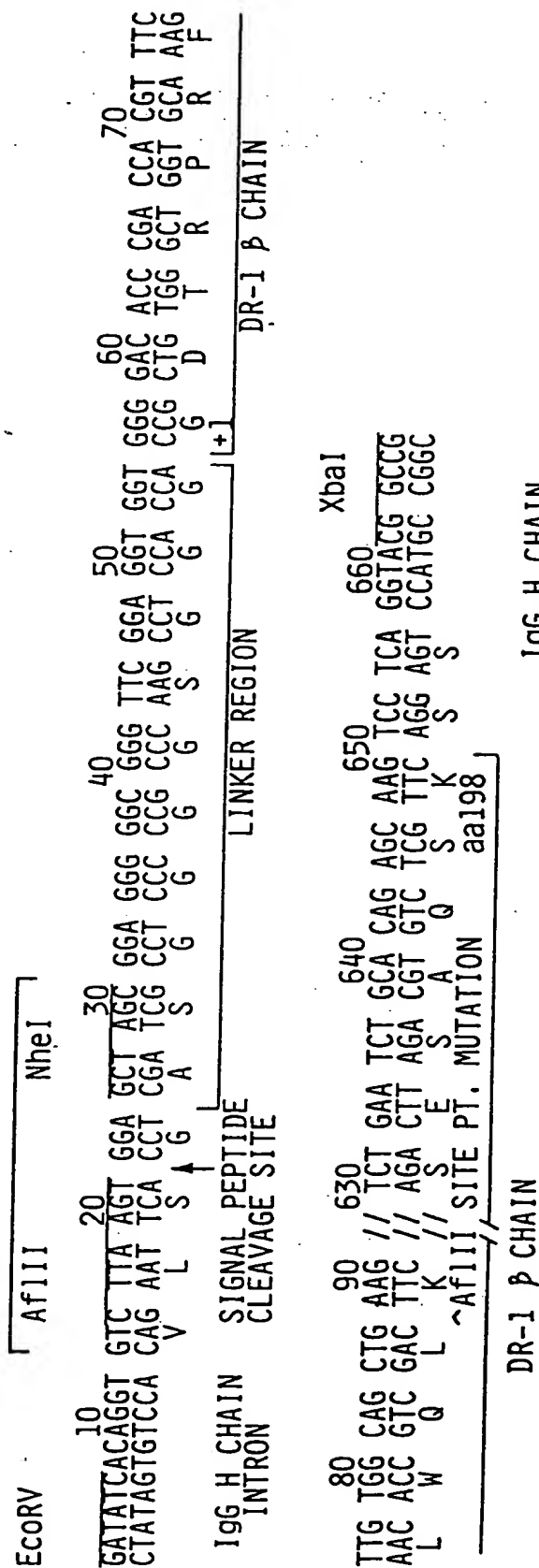






**Fig. 9**

# RESTRICTION SITES FOR INSERTION OF OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST



**Fig. 9F**

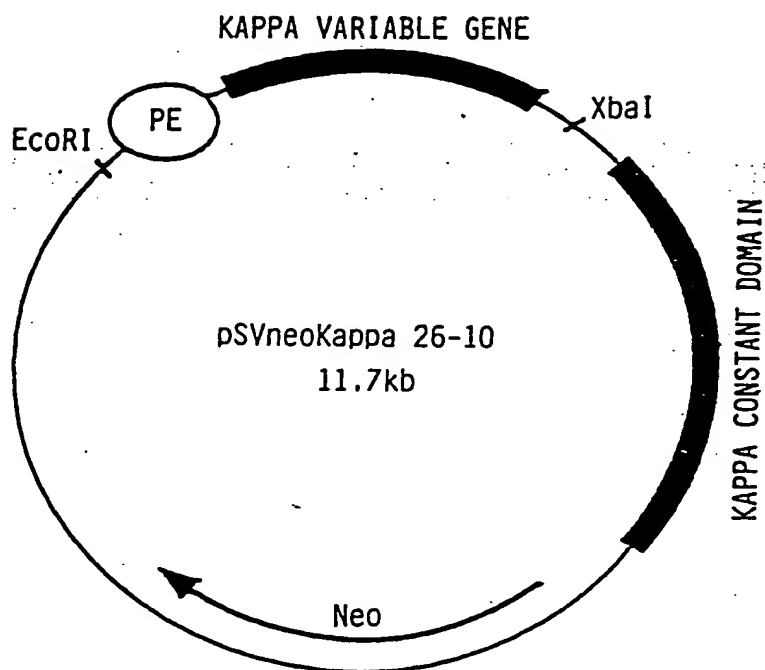


FIG. 10A

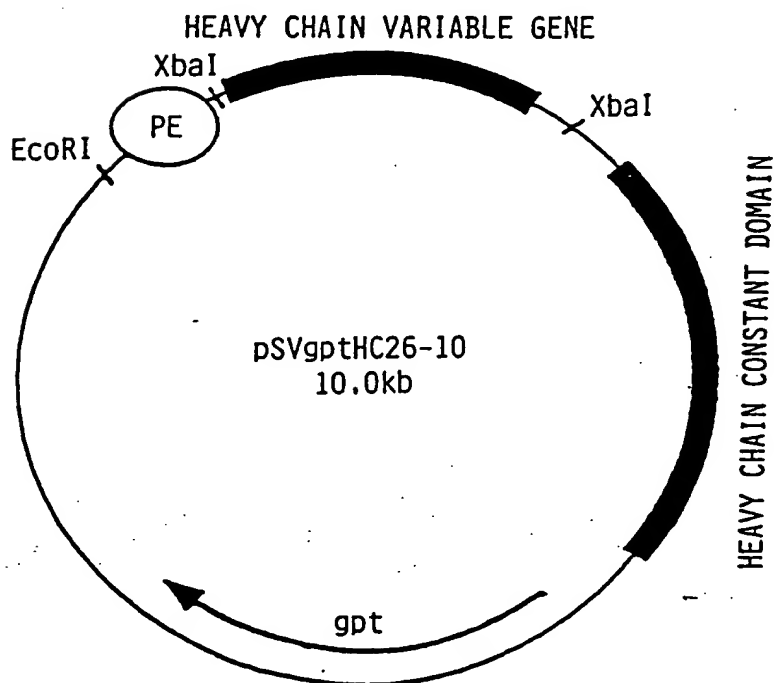


FIG. 10B

0948164-05001

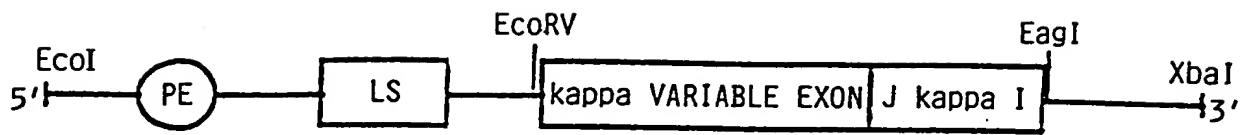


FIG. 11A



FIG. 11B

09848164.050301

0948164-050301  
T06050-49T84860

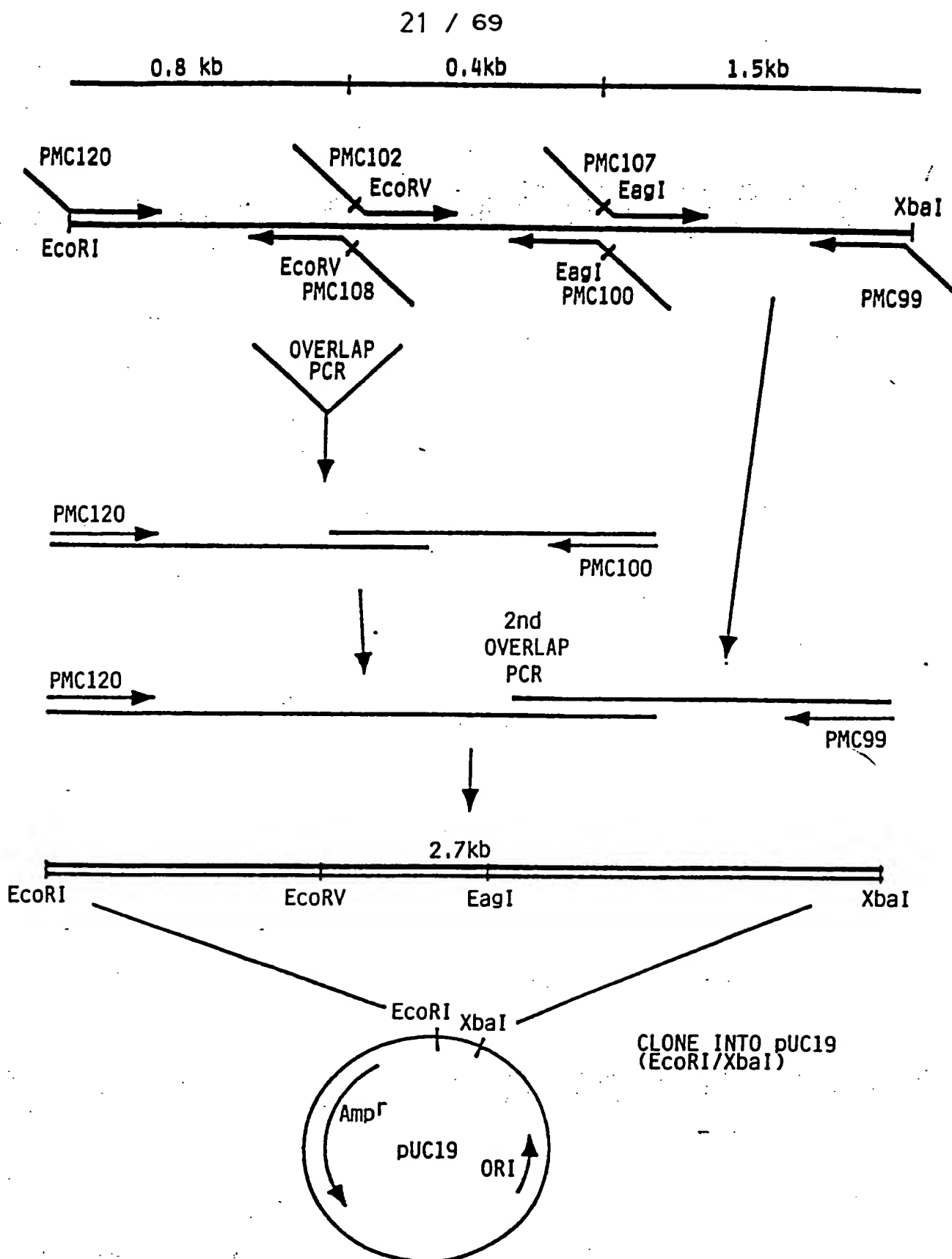


FIG. 12

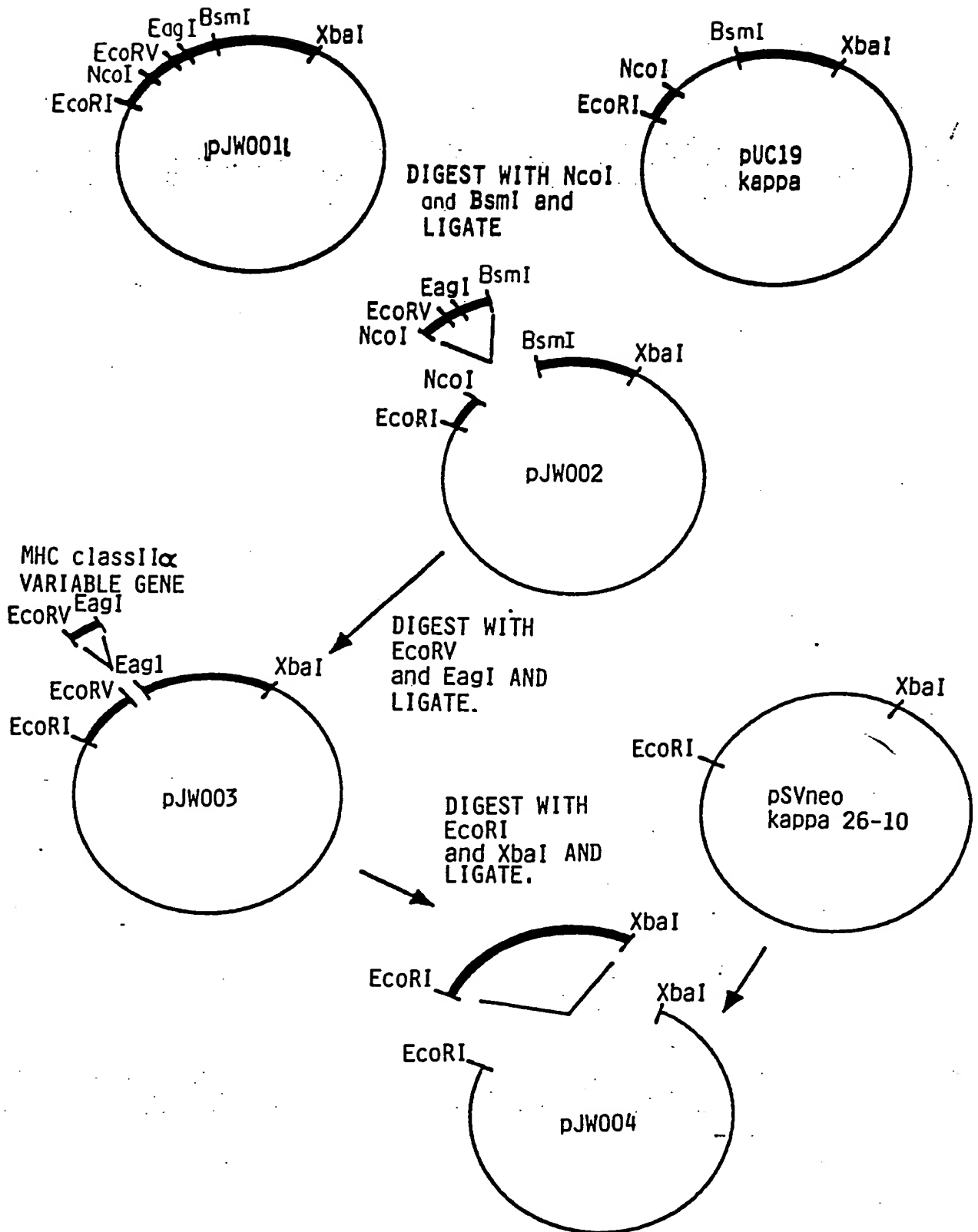


FIG. 13

PRIMER LISTSEQUENCE

PMC-33

[5'GCTCAGCTGTCTTGTTCAGTACTGATC3']

PMC-77

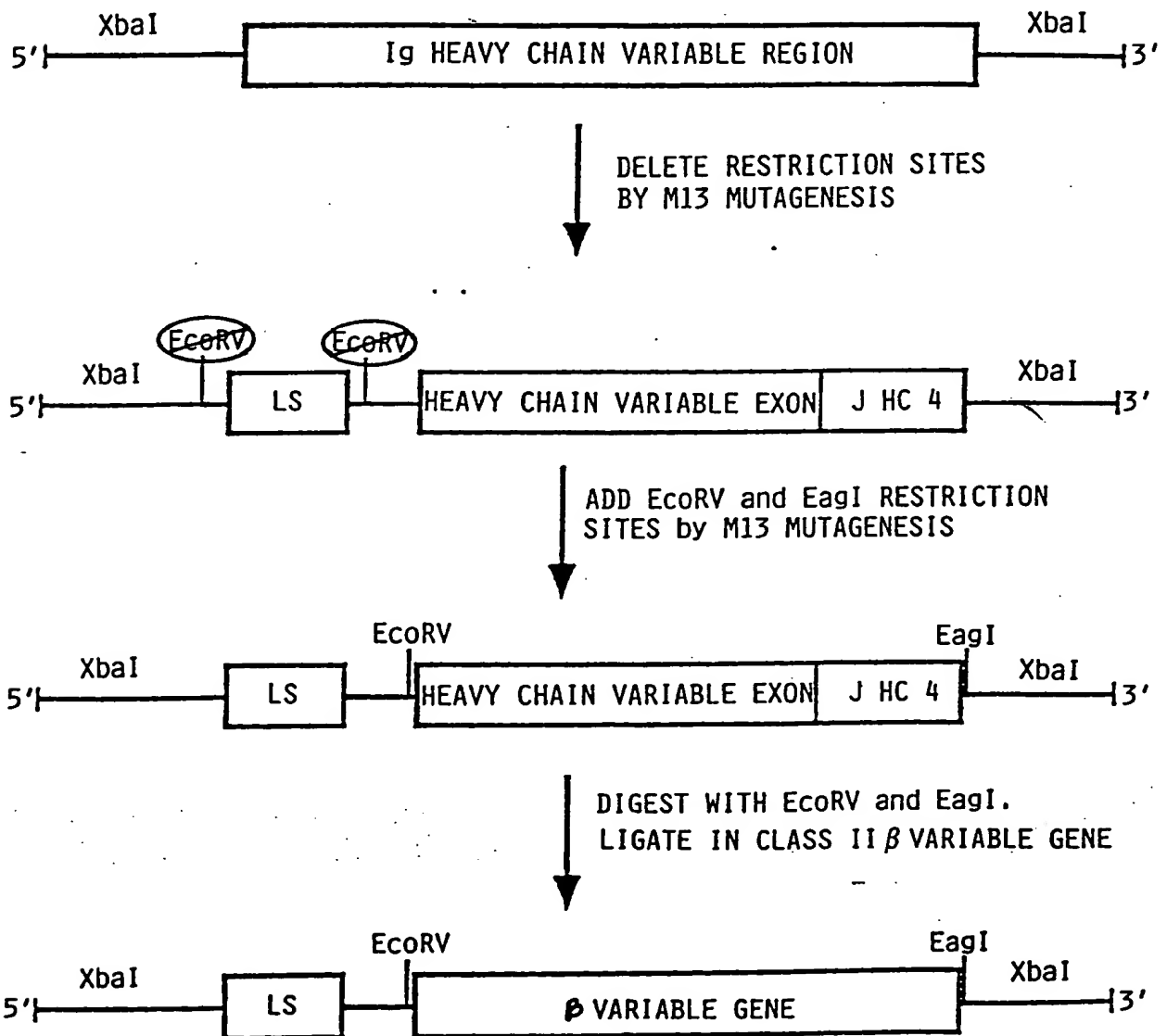
[5'GTAAGTAGCGGCCG3']

PMC-111

[5'GGTATGTAAAAATAAACATCACAG3']

PMC-114

[5'GCTTTGCTTACGGAGTTACTC3']

**FIG. 14****FIG. 15**

09343154.050301

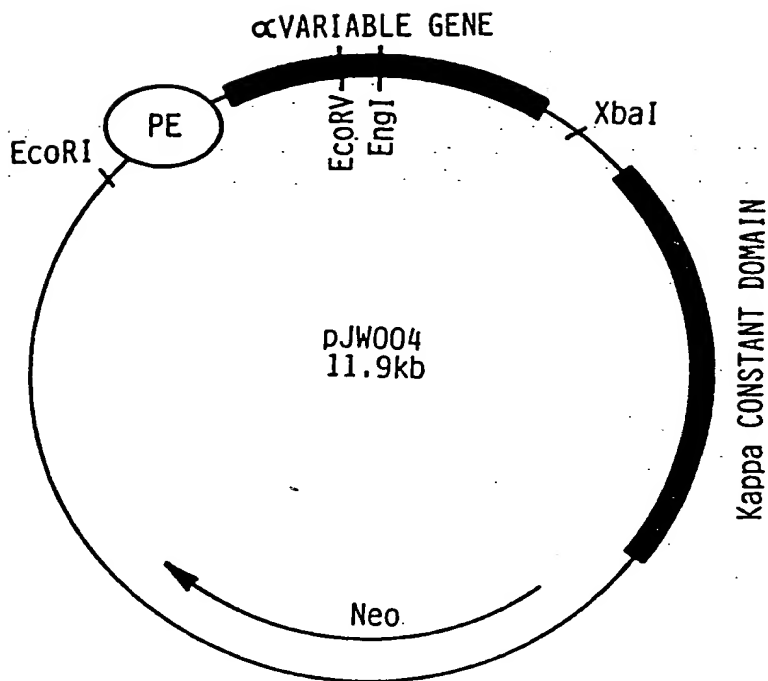


FIG. 16A

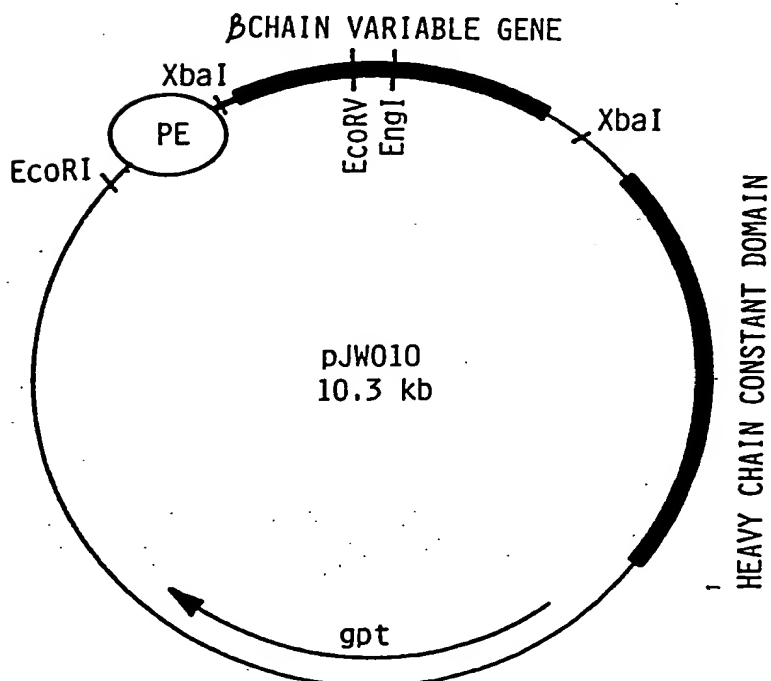


FIG. 16B



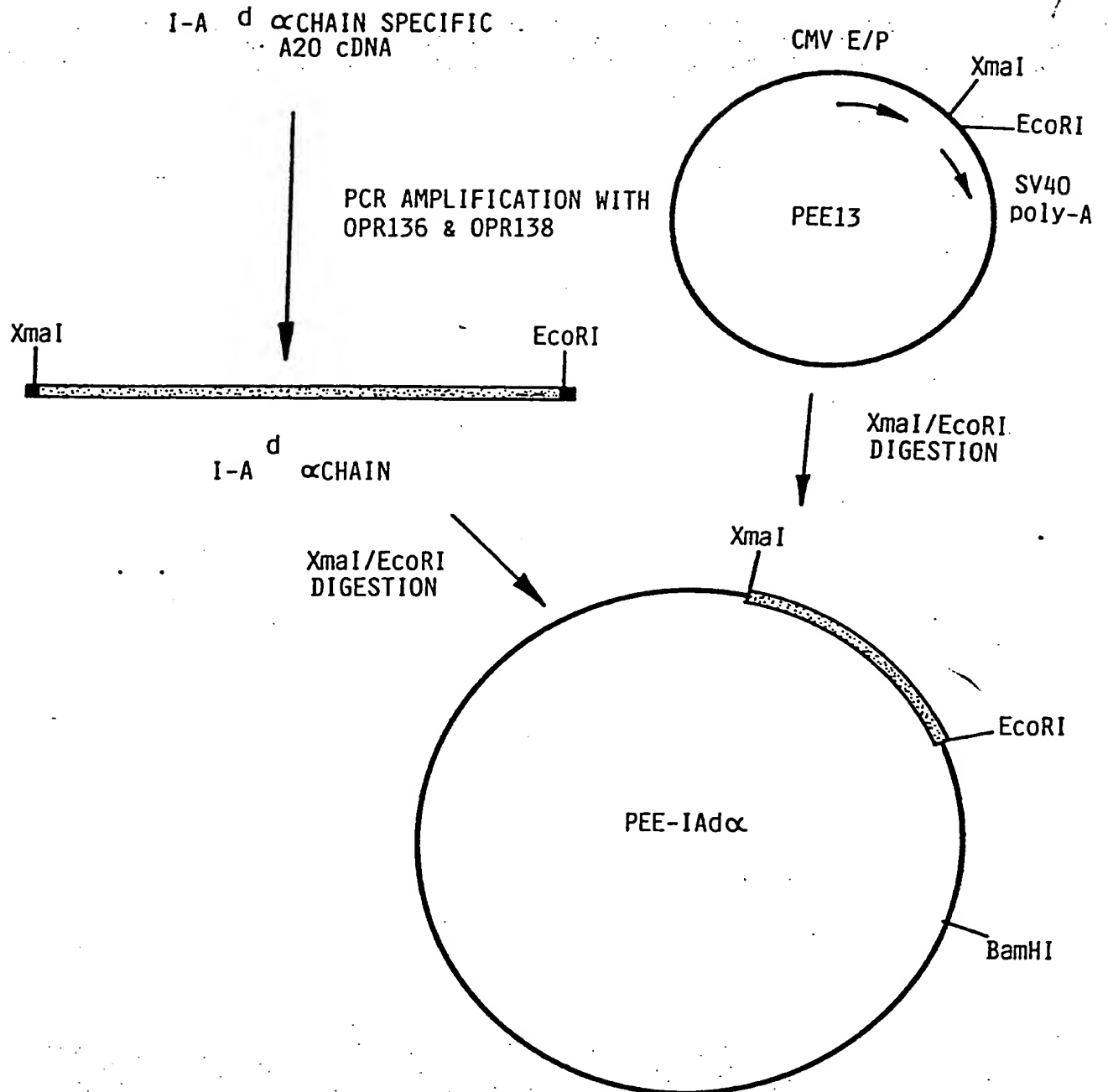


FIG. 17A

094164-050301

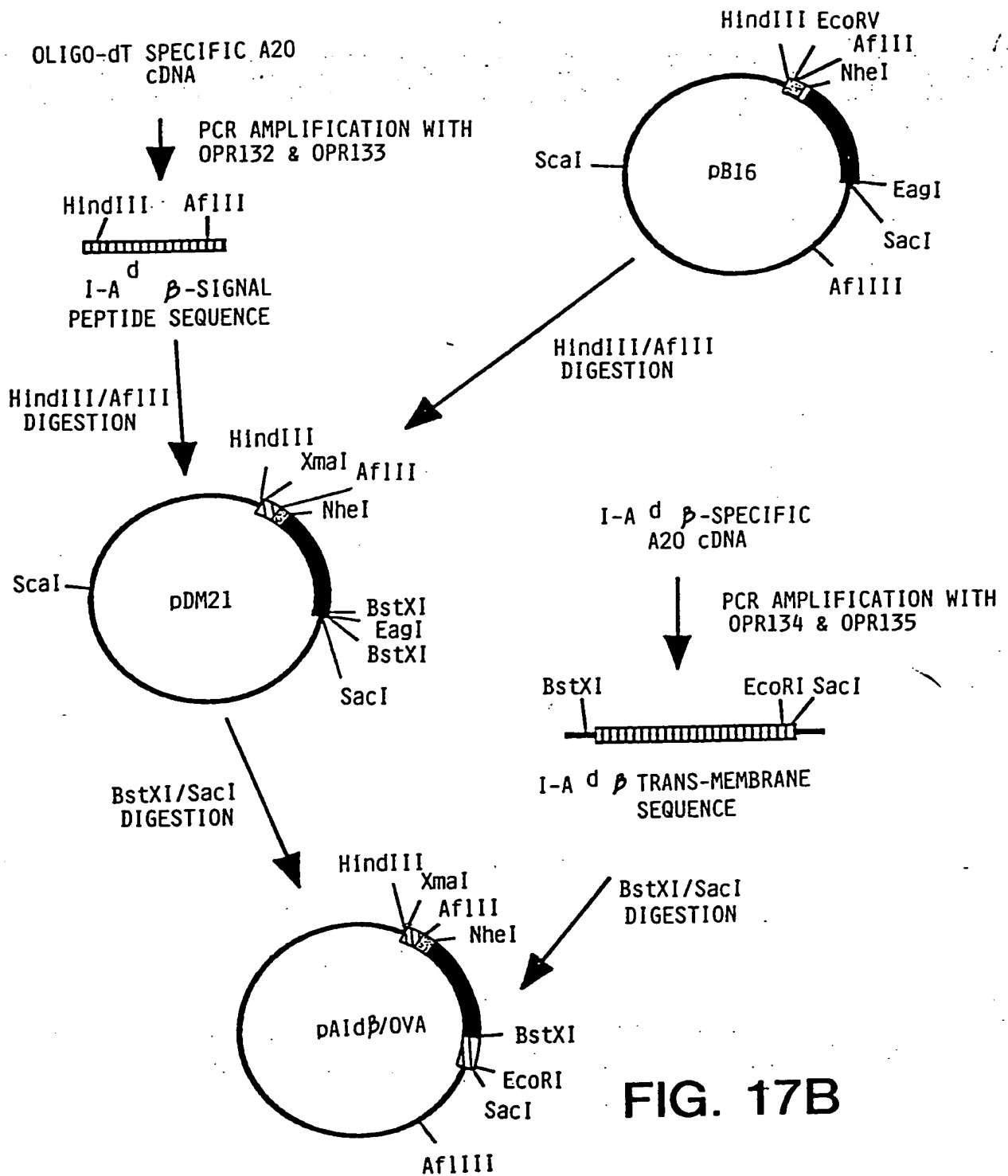


FIG. 17B

09348164.050301

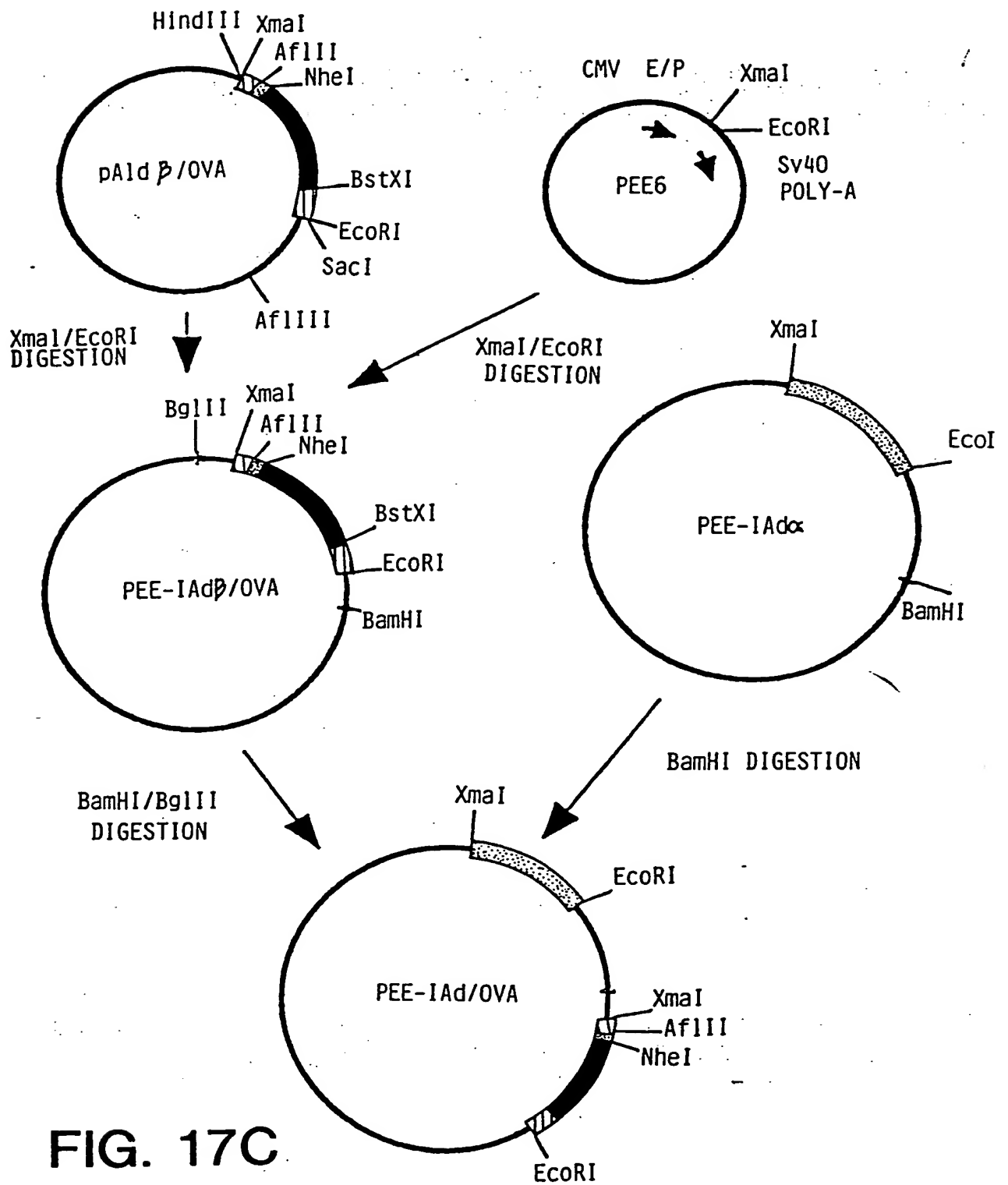


FIG. 17C

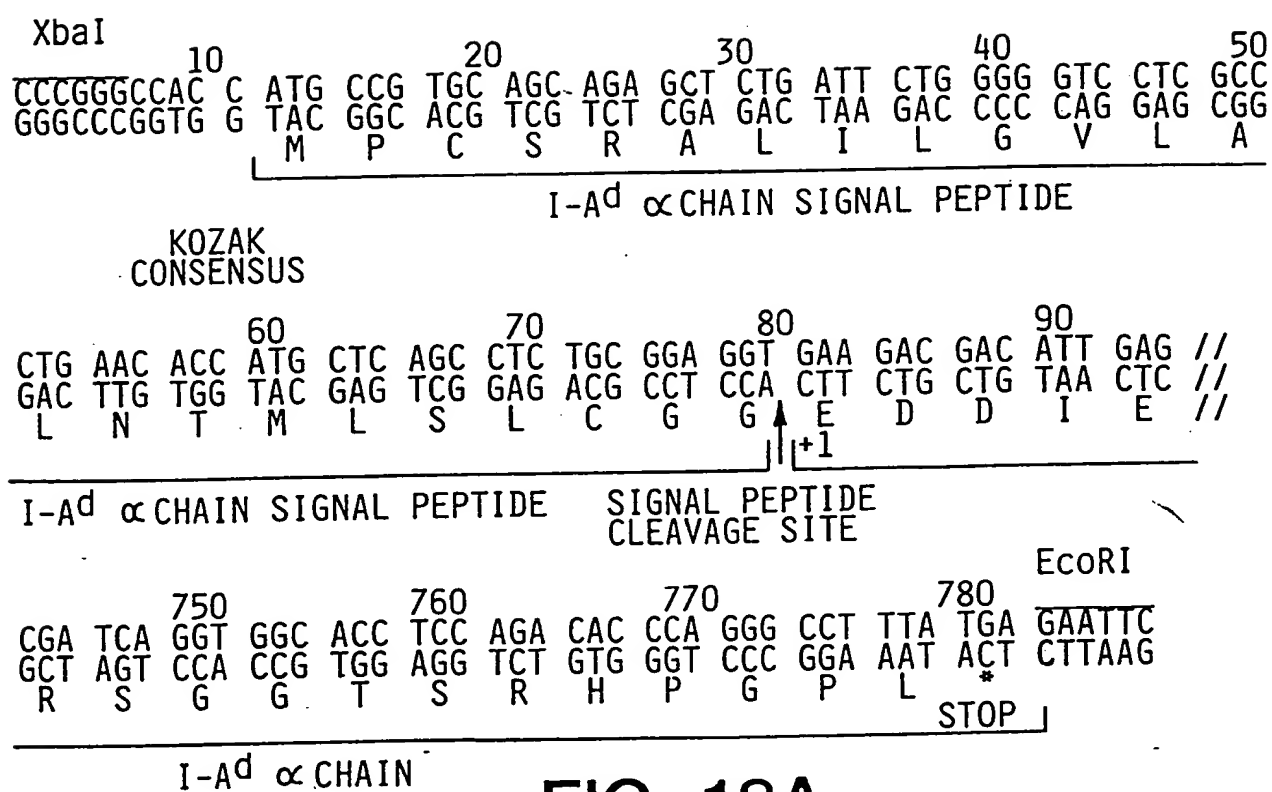


FIG. 18A

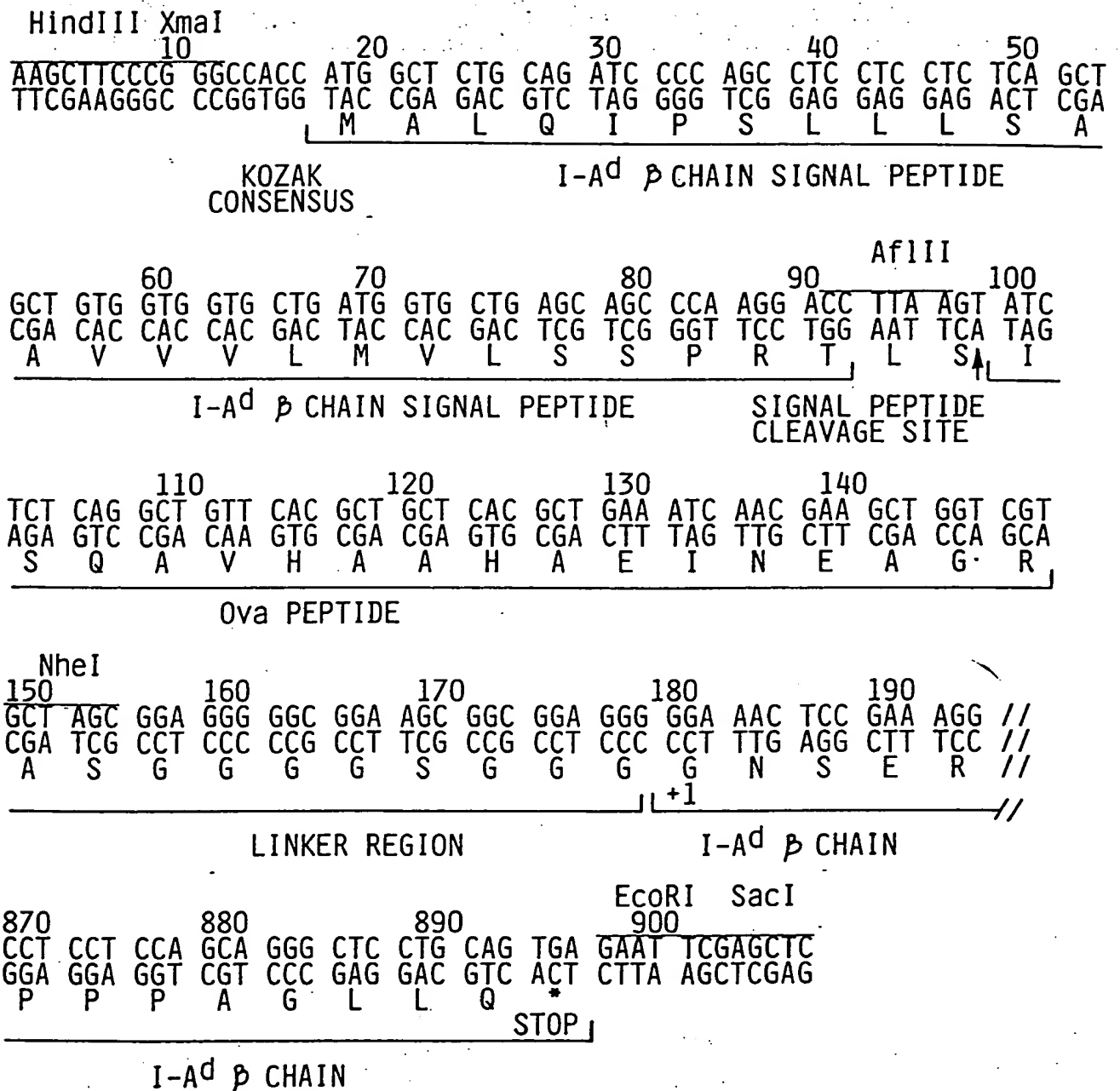


FIG. 18B

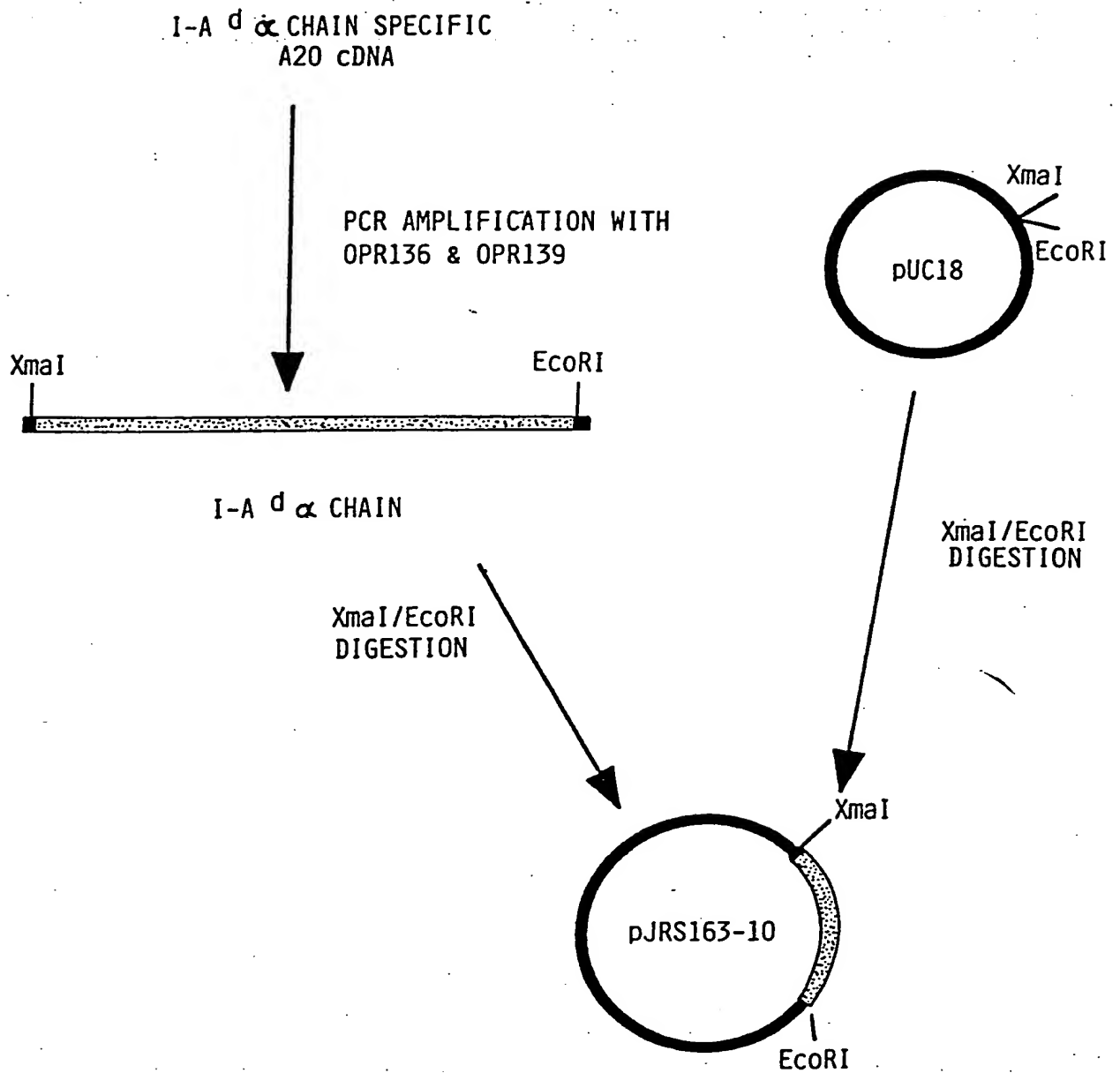


FIG. 19A

09348164-050301

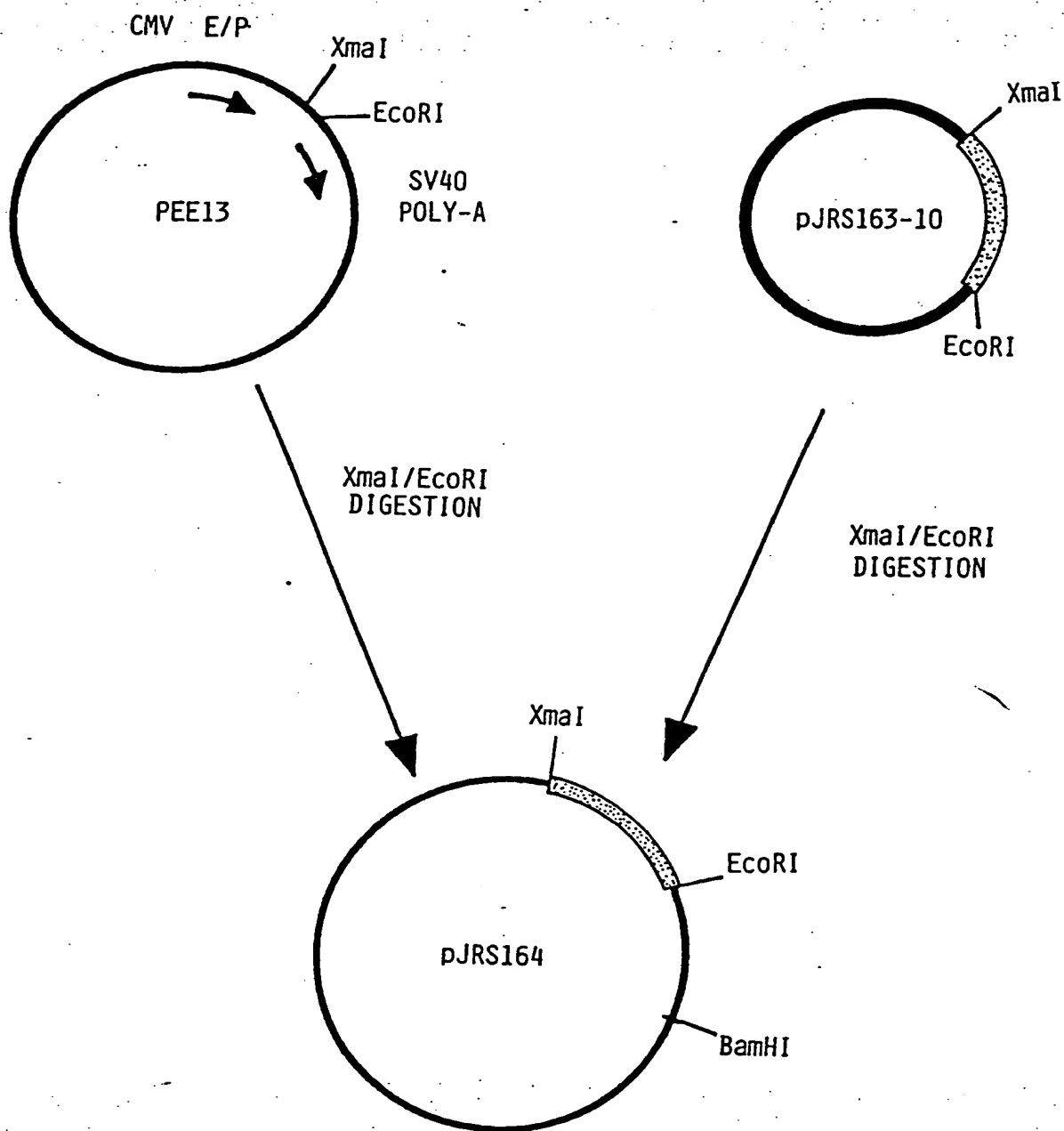


FIG. 19B

0948164.0501  
"450" 4518460

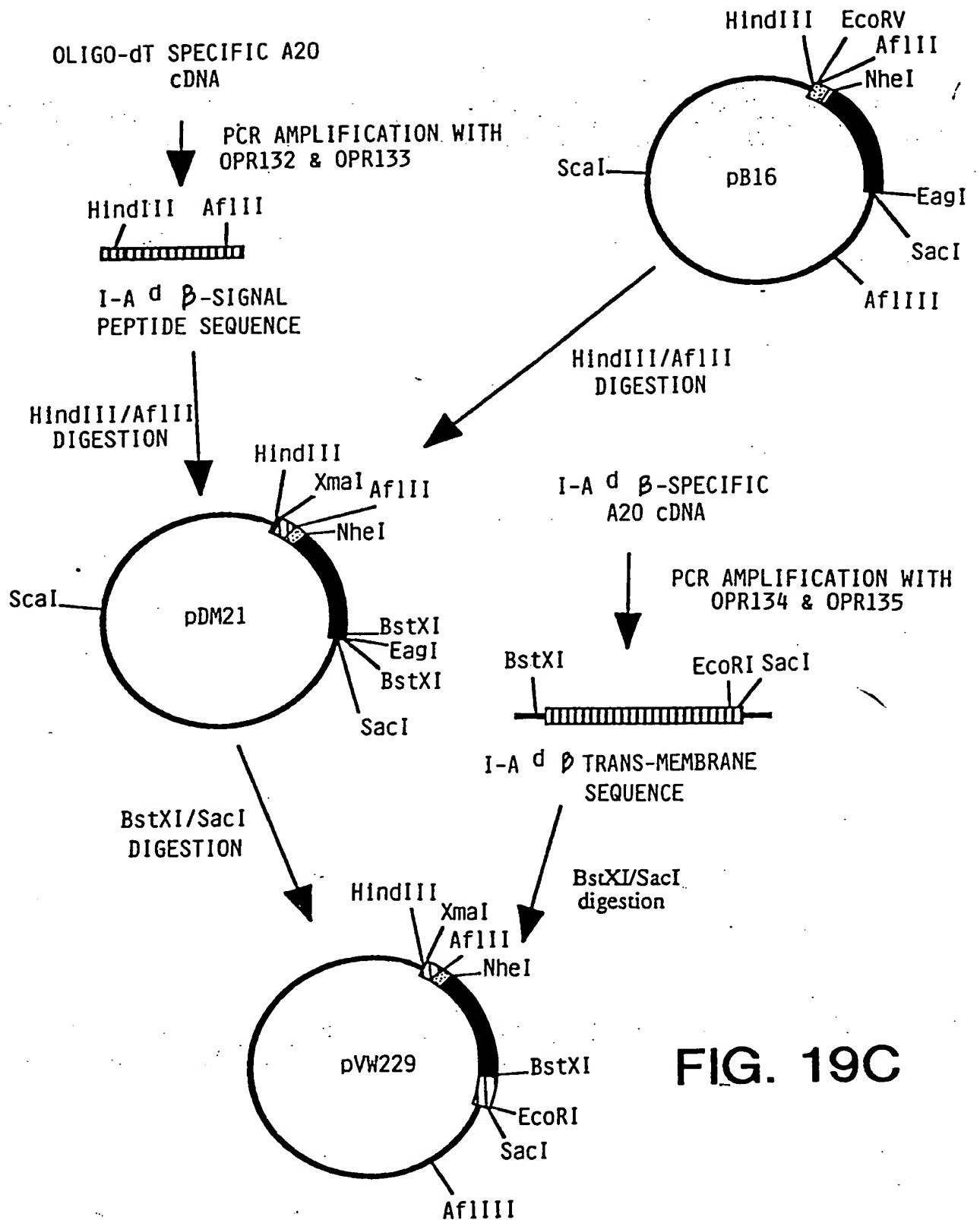


FIG. 19C



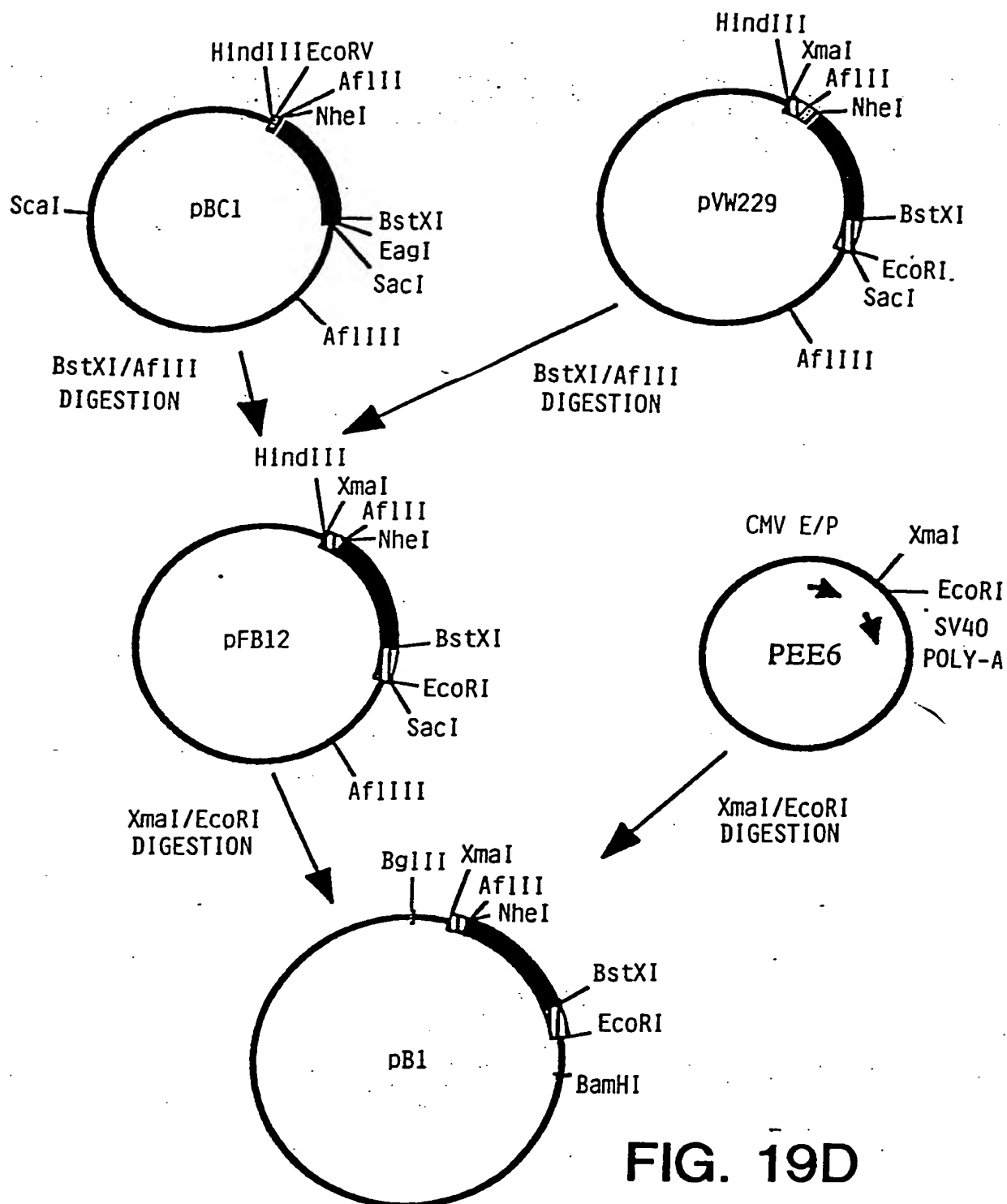


FIG. 19D

09343164.050301

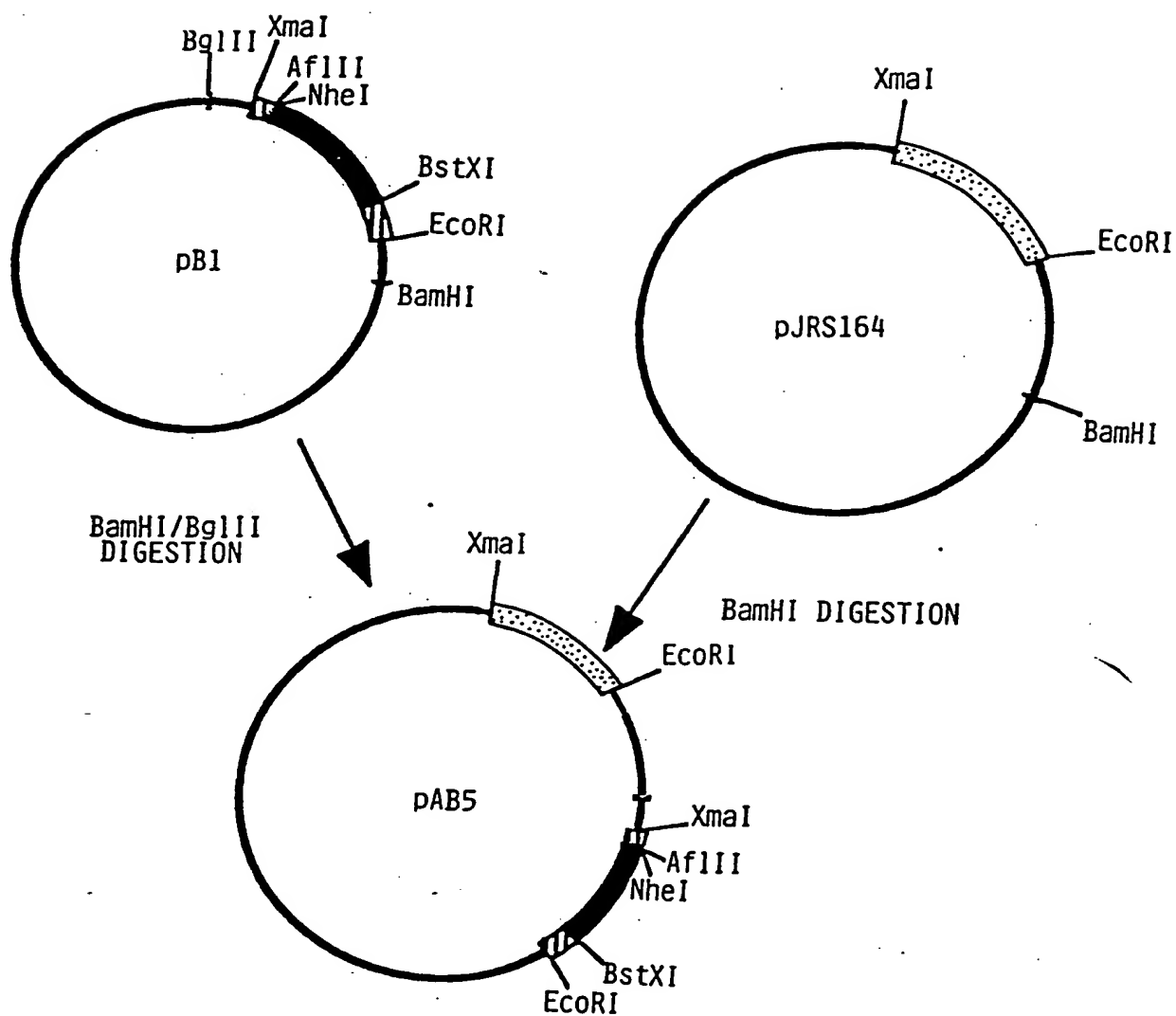
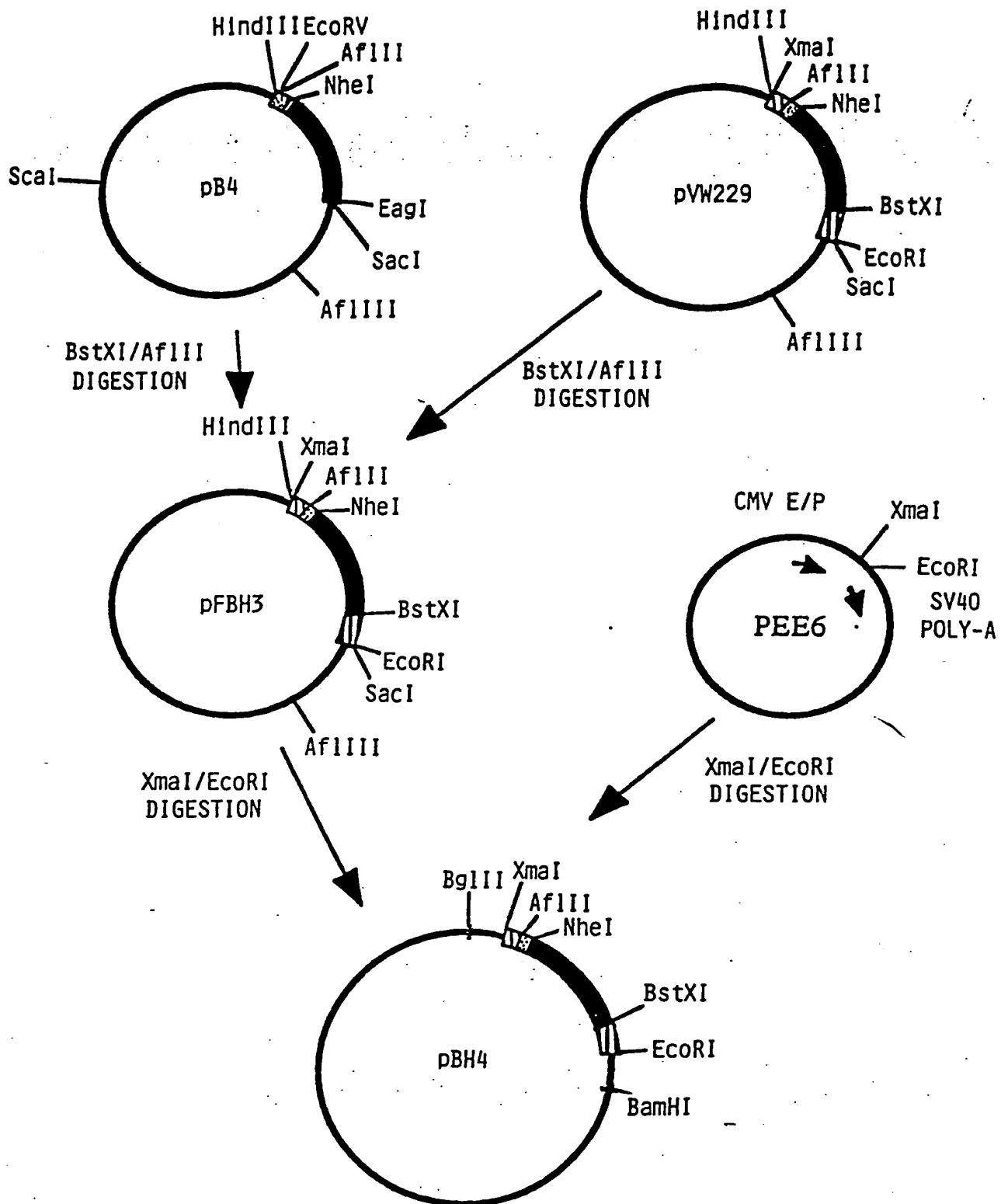


FIG. 19E



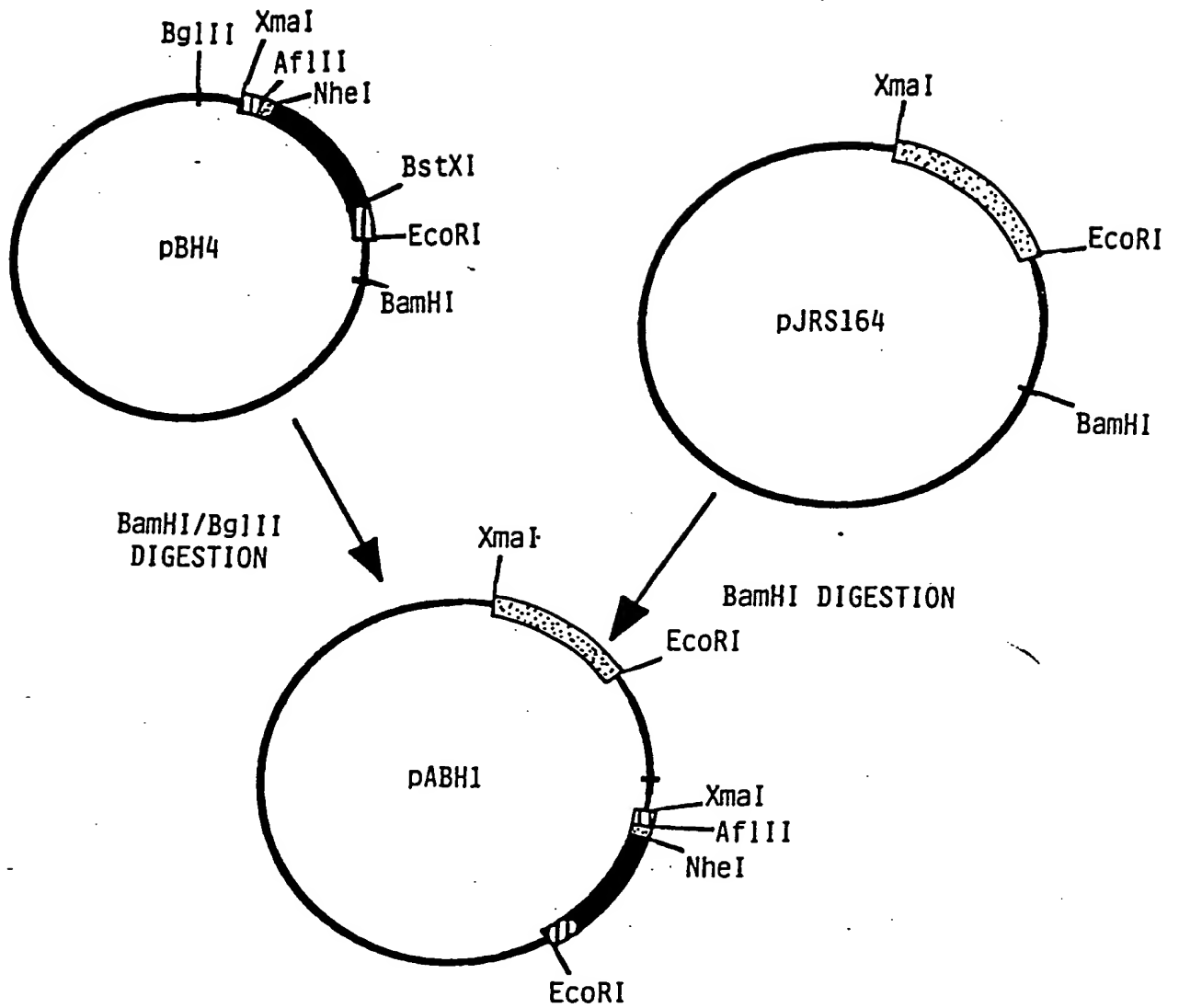


FIG. 19G

0948164.0503

**OPR132**I-A<sup>d</sup>  $\beta$  signal peptide front primer with Kozak consensus for CellTech vector -

HindIII/XmaI sites

5'-CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA  
GC-3'**OPR133**I-A<sup>d</sup>  $\beta$  signal peptide back primer with Kozak consensus for CellTech vector - AflII site5'-CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'**OPR134**I-A<sup>d</sup>  $\beta$  transmembrane front primer for CellTech vector - BstXI sites5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'**OPR135**I-A<sup>d</sup>  $\beta$  transmembrane back primer for CellTech vector - SstI, EcoRI sites5'-CCC CCC GAG CTC GAA TCC TCA CTG CAG GAG CCC TGC TGG-3'**OPR136**I-A<sup>d</sup>  $\alpha$  signal peptide front primer with Kozak consensus for CellTech vector -

HindIII/XmaI sites

5'-CCC CCC AAG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC  
TG-3'**OPR139**I-A<sup>d</sup>  $\alpha$  transmembrane primer for CellTech vector - SstI/EcoRI sites5'-CCC CCC GAG CTC GAA TCC TCA TAA AGG CCC TGG GTG TCT G-3'**B7-1-2F**

Murine B7-1 front primer with Kozak consensus for CloneTech vector - NotI site

5'-CCC CCC CCG CGG CCG CCC CAC CAT GGG ACT GAG TAA CAT TCT  
C-3'**B7-1-2B**

Murine B7-1 BACK primer for CloneTech vector - NotI site

5'-CCC CCC GCG GCC GCT TTA AAA ACA TGT ATC ACT TTT-3'**FIG. 20**

T06050"49T84860

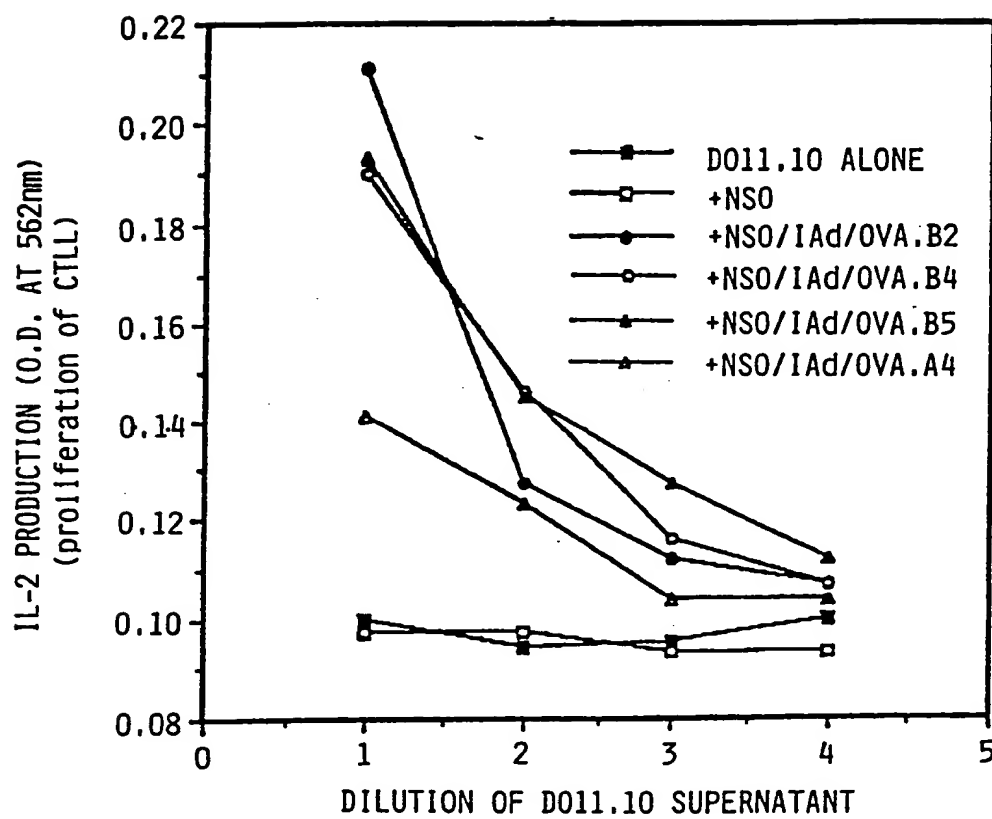


FIG. 21

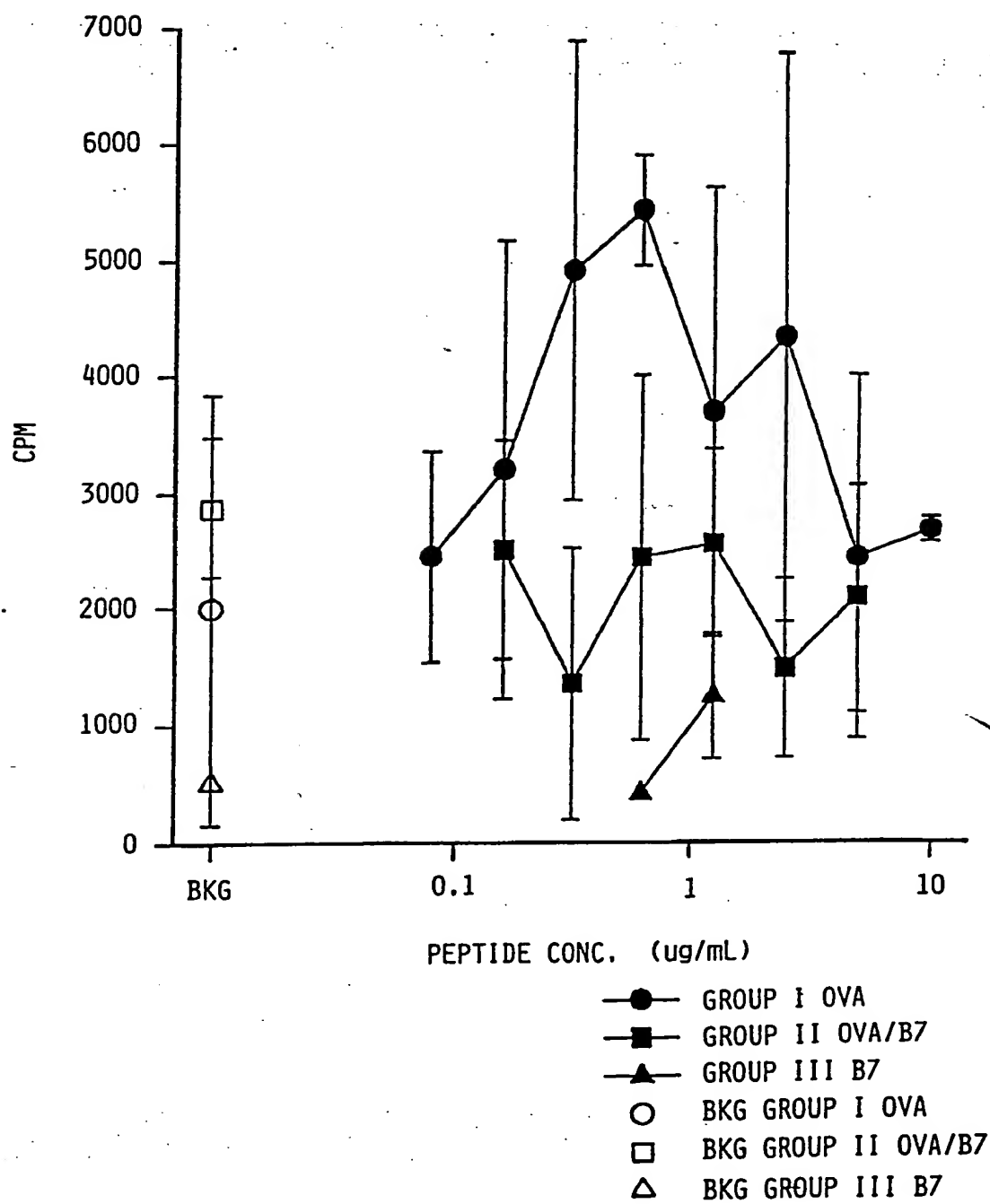


FIG. 22

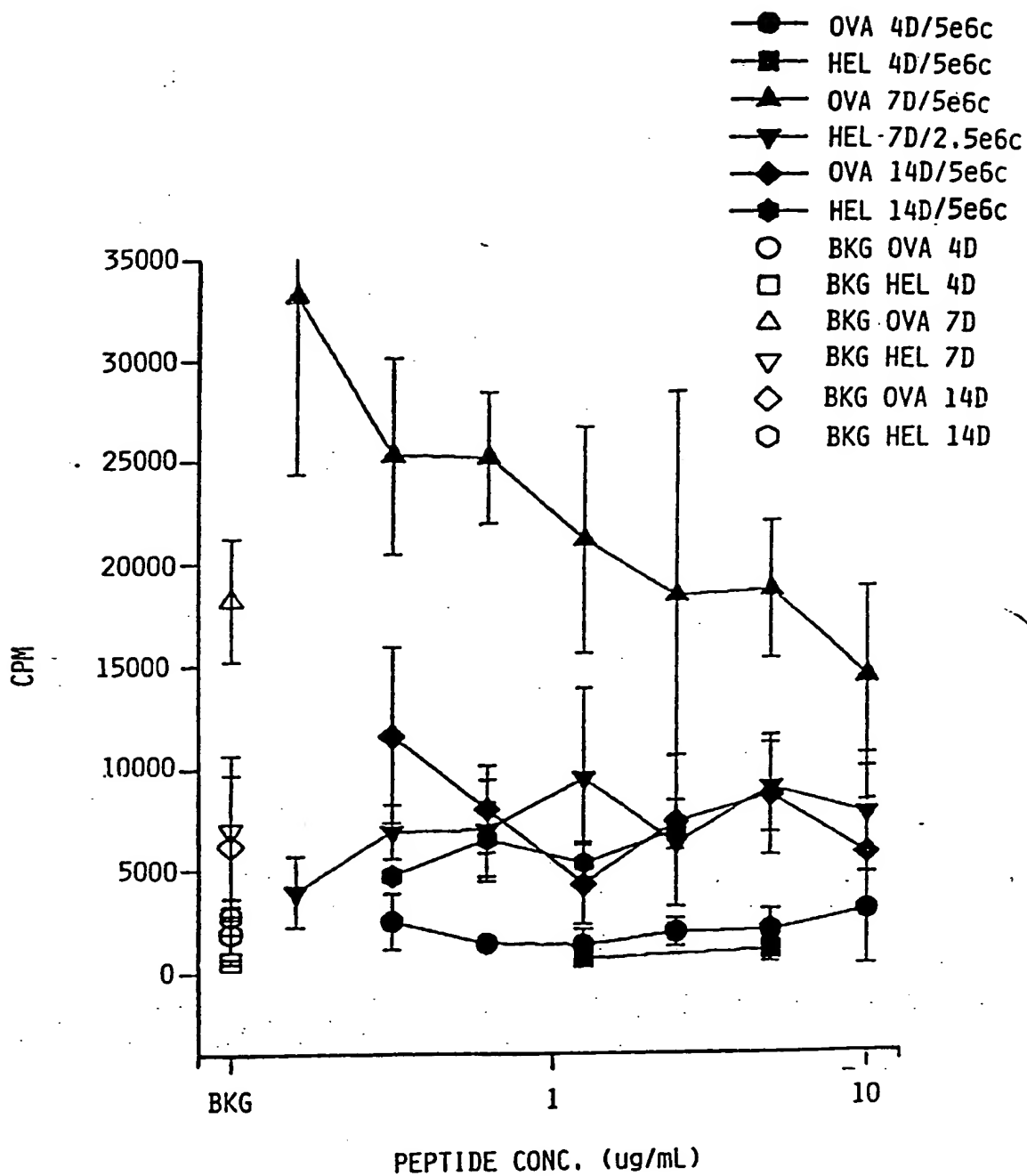


FIG. 23



LINKER SEQUENCE LINKED TO  
PRESENTING PEPTIDE

PEPTIDE BINDING  
GROOVE



α2 DOMAIN

β2 DOMAIN

SINGLE CHAIN  
LINKER SEQUENCE

FIG.24

0948164.050304  
T0E050"49T87260

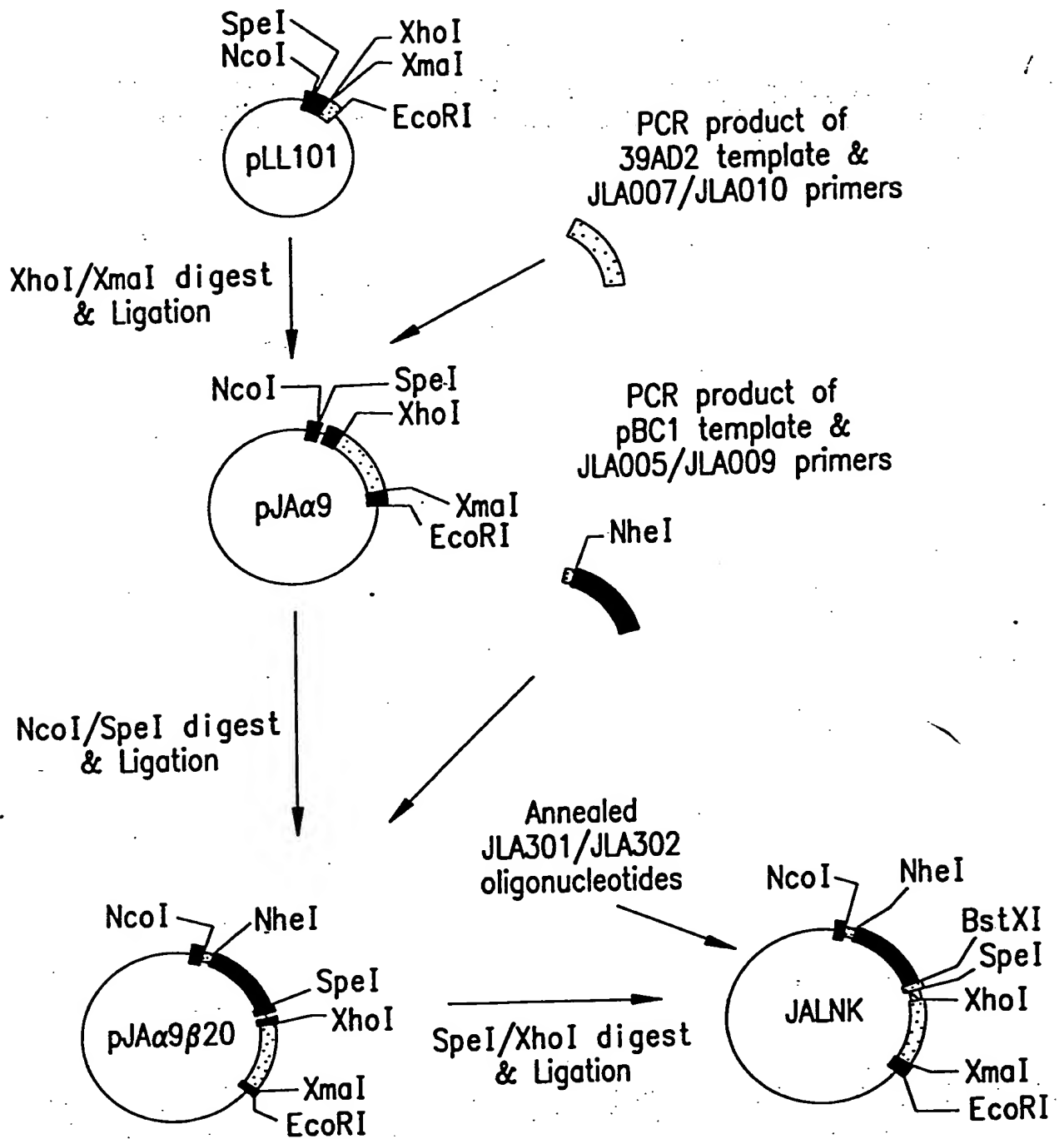


FIG.25A

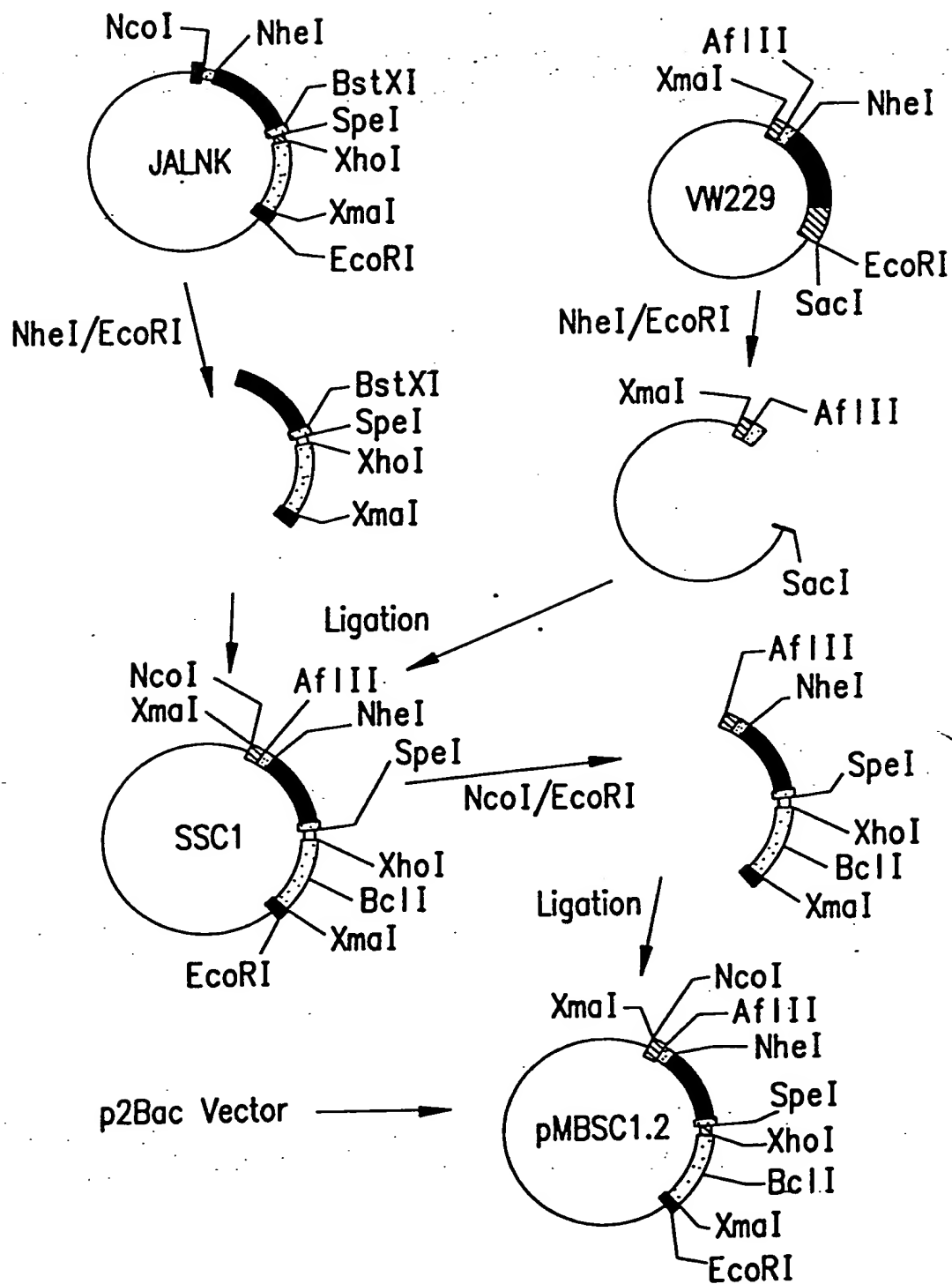


FIG. 25B

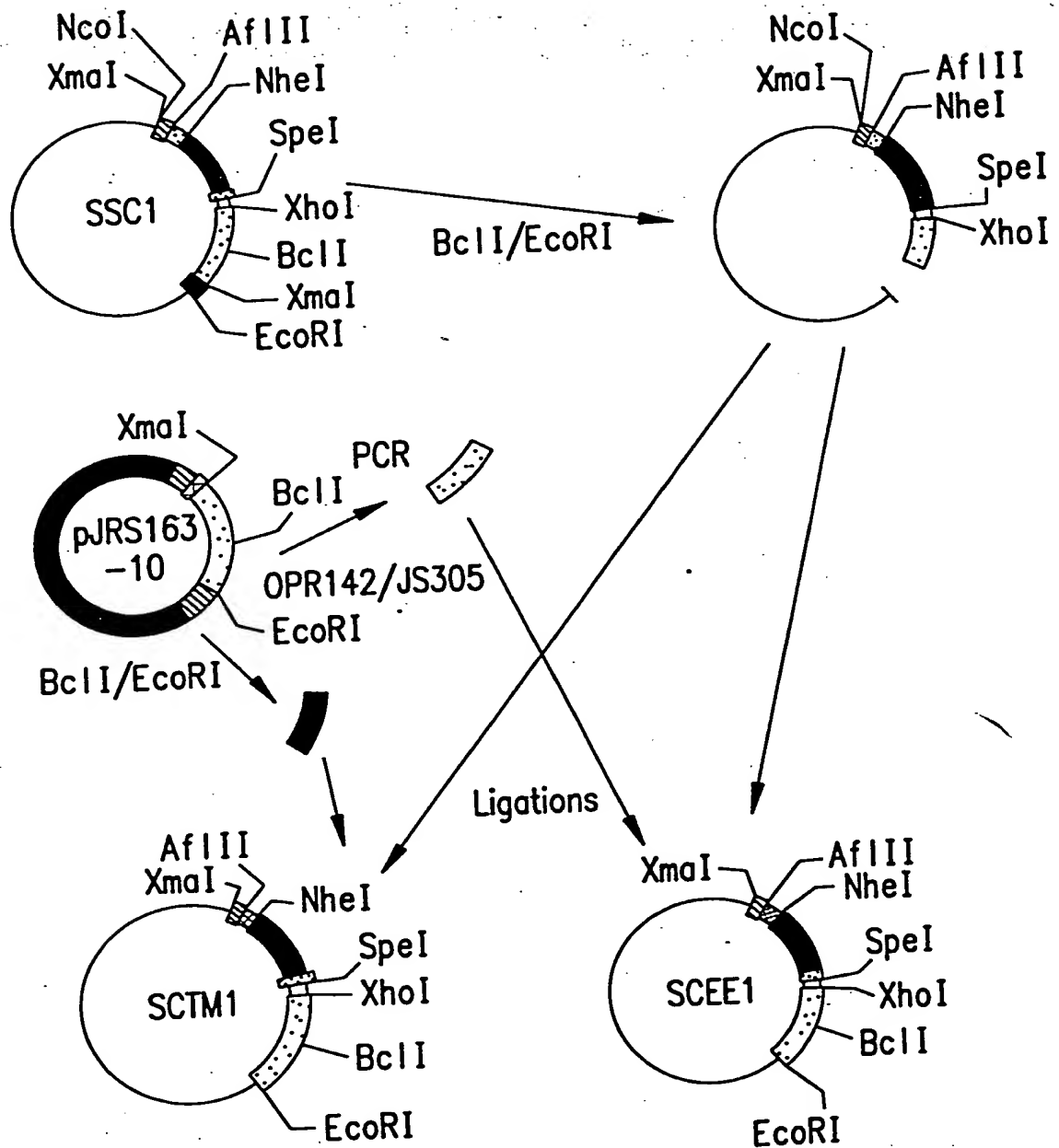


FIG.25C

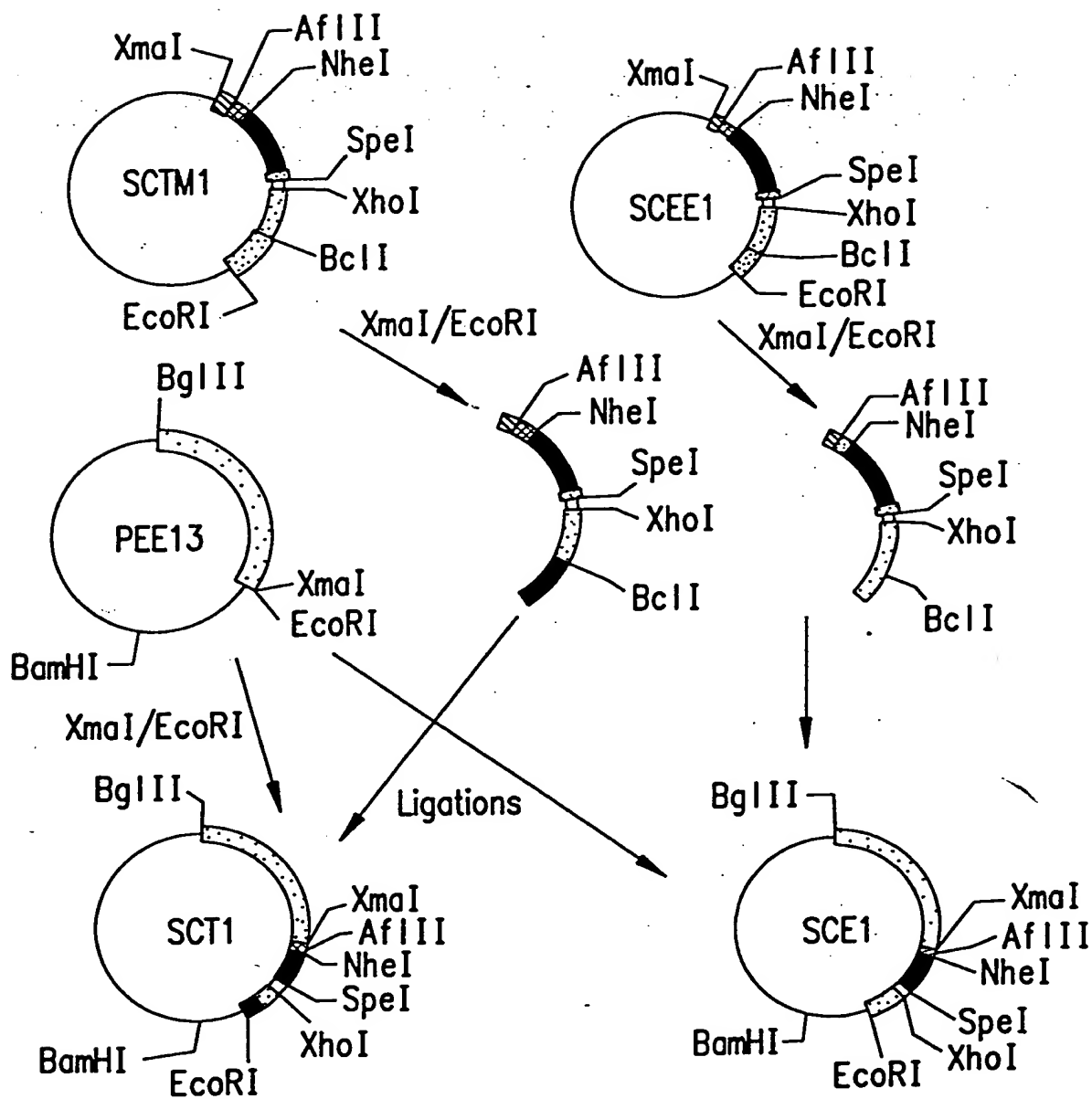


FIG.25D

JLA-005

5' -CCCCCGCCATGGCCGCTAGCGGAGGGGGCGGAAGC-3'

JLA-007

5' -CCCGGGGCTCGAGTGAAGACGACATTGAGGCCGAC-3'

JLA-009

5' -CCCCCACTAGTCCACTCCACAGTGATGGGGCT-3'

JLA-010

5' -CCCCCCCCCGGGACCAAGTGTTTCAGAACCGGCTCCTC-3'

JLA-301

5' -TCGAGGAACCGCCACCGCCAGAACCGCCGCCACCGGA-  
ACCACCACCGCCGCTGCCACCGCCACCA-3'

JLA-302

5' -CTAGTGGTGGCGGTGGCAGCGGCGGTGGTGGTTCCGG-  
TGGCGGCGGTCTGGCGGTGGCGGTTCC-3'

OPR-142

5' -CTTGGGAATCTTGACTAAGAGG-3'

JS-305

5' -CAGGTCGAATTCTCATTCCATCGGCATGTACTCTTCTT-  
CCTCCCAGTGTTCAGAACCGG-3'

FIG.26

09848164-050301

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10	20	30	40	50
*	*	*	*	*
CCACC	ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG			
GGTGG	TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC			
	M A L Q I P S L L L S A A V V>			
<----- I-Ad $\beta$ -CHAIN LEADER ----->				
60	70	80	90	
*	*	*	*	
GTG CTG	ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT			
CAC GAC	TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA			
V L M V L S S P R T L S I S Q A>				
-----				
100	110	120	130	140
*	*	*	*	*
GTT CAC	GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA			
CAA GTG	CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT			
V H A A H A E I N E A G R A S G>				
----- OVA 323-339 -----><-----				
150	160	170	180	190
*	*	*	*	*
GGG GGC	GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC			
CCC CCG	CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG			
G G G S G G G G N S E R H F V V>				
-- 10 AMINO ACID LINKER--><----- I-Ad $\beta$ -1 DOMAIN -----				
200	210	220	230	240
*	*	*	*	*
CAG TTC	AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG			
GTC AAG	TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC			
Q F K G E C Y Y T N G T Q R I R>				
-----				
250	260	270	280	290
*	*	*	*	*
CTC GTG	ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC			
GAG CAC	TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG			
L V T R Y I Y N R E E Y V R Y D>				
-----				

FIG.27A

300                      310                      320                      330  
 \*                      \*                      \*                      \*  
 AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC  
 TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG  
 S D V G E Y R A V T E L G R P D>

340                      350                      360                      370                      380  
 \*                      \*                      \*                      \*                      \*  
 GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC  
 CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG  
 A E Y W N S Q P E I L E R T R A>

390                      400                      410                      420                      430  
 \*                      \*                      \*                      \*                      \*  
 GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC  
 CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG  
 E V D T A C R H N Y E G P E T S>

440                      450                      460                      470                      480  
 \*                      \*                      \*                      \*                      \*  
 ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC  
 TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG  
 T S L R R L E Q P N V A I S L S>  
 --- I-Ad  $\beta$ -1 DOMAIN --><----- I-Ad  $\beta$ -2 DOMAIN -----

490                      500                      510                      520                      530  
 \*                      \*                      \*                      \*                      \*  
 AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA  
 TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT  
 R T E A L N H H N T L V C S V T>

540                      550                      560                      570  
 \*                      \*                      \*                      \*  
 GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG  
 CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC  
 D F Y P A K I K V R W F R N G Q>

FIG. 27B

09648164.050301



580				590				600				610				620
*				*				*				*				*
GAG	GAG	ACA	GTG	GGG	GTC	TCA	TCC	ACA	CAG	CTT	ATT	AGG	AAT	GGG	GAC	
CTC	CTC	TGT	CAC	CCC	CAG	AGT	AGG	TGT	GTC	GAA	TAA	TCC	TTA	CCC	CTG	
E	E	T	V	G	V	S	S	T	Q	L	I	R	N	G	D>	

630			640			650			660			670			
*			*			*			*			*			
TGG	ACC	TTC	CAG	GTC	CTG	GTC	ATG	CTG	GAG	ATG	ACC	CCT	CAT	CAG	GGA
ACC	TGG	AAG	GTC	CAG	GAC	CAG	TAC	GAC	CTC	TAC	TGG	GGA	GTA	GTC	CCT
W	T	F	Q	V	L	V	M	L	E	M	T	P	H	Q	G>

680	690	700	710	720
*	*	*	*	*
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC				
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG				
E V Y T C H V E H P S L K S P I>				
-----			I-Ad β-2 DOMAIN	-----

730				740				750				760				770	
*				*				*				*				*	
ACT	GTG	GAG	TGG	ACT	AGT	GGT	GGC	GGT	GGC	AGC	GGC	GGT	GGT	GGT	TCC		
TGA	CAC	CTC	ACC	TGA	TCA	CCA	CCG	CCA	CCG	TGC	CCG	CCA	CCA	CCA	AGG		
T	V	E	W	T	S	G	G	G	G	S	G	G	G	G	S		
-----><-----																24 AMINO ACID LINKER -----	

780				790				800				810			
*				*				*				*			
GGT	GGC	GGC	GGT	TCT	GGC	GGT	GGC	GGT	TCC	TCG	AGT	GAA	GAC	GAC	ATT
CCA	CCG	CCG	CCA	AGA	CCG	CCA	CCG	CCA	AGG	AGC	TCA	CTT	CTG	CTG	TAA
G	G	G	G	S	G	G	G	G	S	S	S	E	D	D	I>

```

820          830          840          850          860
  *            *            *            *            *
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
  E   A   D   H   V   G   F   Y   G   T   T   V   Y   Q   S   P>
----- I-Ad α-1 DOMAIN -----

```

FIG. 27C

870                      880                      890                      900                      910  
 \*                      \*                      \*                      \*                      \*  
 GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC  
 CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG  
 G D I G Q Y T H E F D G D E L F>

920                      930                      940                      950                      960  
 \*                      \*                      \*                      \*                      \*  
 TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT  
 ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA  
 Y V D L D K K K T V W R L P E F>

970                      980                      990                      1000                      1010  
 \*                      \*                      \*                      \*                      \*  
 GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT  
 CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA  
 G Q L I L F E P Q G G L Q N I A>

1020                      1030                      1040                      1050  
 \*                      \*                      \*                      \*  
 GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC  
 CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG  
 A E K H N L G I L T K R S N F T>  
 ----- I-Ad  $\alpha$ -1 DOMAIN -----

1060                      1070                      1080                      1090                      1100  
 \*                      \*                      \*                      \*                      \*  
 CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT  
 GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA  
 P A T N E A P Q A T V F P K S P>  
 -----><----- I-Ad  $\alpha$ -2 DOMAIN -----

1110                      1120                      1130                      1140                      1150  
 \*                      \*                      \*                      \*                      \*  
 GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC  
 CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG  
 V L L G Q P N T L I C F V D N I>

FIG.27D

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 10E050 49T84850

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1160	1170	1180	1190	1200
*	*	*	*	*
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC				
AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG				
F P P V I N I T W L R N S K S V>				
-----				
1210	1220	1230	1240	1250
*	*	*	*	*
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC				
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG				
T D G V Y E T S F L V N R D H S>				
-----				
1260	1270	1280	1290	
*	*	*	*	
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT				
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA				
F H K L S Y L T F I P S D D D I>				
-----				
1300	1310	1320	1330	1340
*	*	*	*	*
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA				
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT				
Y D C K V E H W G L E E P V L K>				
----- I-Ad $\alpha$ -2 DOMAIN -----				
1350	1360	1370	1380	
*	*	*	*	
CAC TGG TCC CGG GCT AGT CAC CAT CAC CAT CAT CAC TAG				
GTG ACC AGG GCC CGA TCA GTG GTA GTG GTA GTA GTG ATC				
H W S R A S H H H H H H >				
-----><----- 6 X HIS tag ----->				

FIG.27E

09043164-050301

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10 20 30 40 50  
\* \* \* \* \*  
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG  
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC  
M A L G I P S L L L S A A V V>  
----- I-Ad β CHAIN LEADER -----

60 70 80 90  
\* \* \* \* \*  
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT  
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA  
V L M V L S S P R T L S I S Q A>  
-----><-----

100 110 120 130 140  
\* \* \* \* \*  
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA  
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT  
V H A A H A E I N E A G R A S G>  
-----><-----  
OVA 323-339

150 160 170 180 190  
\* \* \* \* \*  
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC  
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG  
G G G S G G G G N S E R H F V V>  
-- 10 AMINO ACID LINKER --><----- I-Ad β-1 DOMAIN -----

200 210 220 230 240  
\* \* \* \* \*  
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG  
GTC AAG TTC CCG CTC ACG ATG ATG TCC TTG CCC TGC GTC GCG TAT GCC  
Q F K G E C Y Y T N G T Q R I R>  
-----

250 260 270 280 290  
\* \* \* \* \*  
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC  
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG  
L V T R Y I Y N R E E Y V R Y D>  
-----

FIG.28A

000050"49T84B60

300                      310                      320                      330  
 \*                      \*                      \*                      \*  
 AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC  
 TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG  
 S D V G E Y R A V T E L G R P D>

---

340                      350                      360                      370                      380  
 \*                      \*                      \*                      \*                      \*  
 GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC  
 CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG  
 A E Y W N S Q P E I L E R T R A>

---

390                      400                      410                      420                      430  
 \*                      \*                      \*                      \*                      \*  
 GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC  
 CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG  
 E V D T A C R H N Y E G P E T S>

---

440                      450                      460                      470                      480  
 \*                      \*                      \*                      \*                      \*  
 ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC  
 TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG  
 T S L R R L E Q P N V A I S L S>  
 --- I-Ad  $\beta$ -1 DOMAIN -><----- I-Ad  $\beta$ -2 DOMAIN -----

---

490                      500                      510                      520                      530  
 \*                      \*                      \*                      \*                      \*  
 AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA  
 TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT  
 R T E A L N H H N T L V C S V T>

---

540                      550                      560                      570  
 \*                      \*                      \*                      \*  
 GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG  
 CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC  
 D F Y P A K I K V R W F R N G Q>

---

FIG.28B

0948164-050304

580 \* 590 \* 600 \* 610 \* 620 \*  
 GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC  
 CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG  
 E E T V G V S S T Q L I R N G D>  
 -----  
 630 \* 640 \* 650 \* 660 \* 670 \*  
 TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA  
 ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT  
 W T F Q V L V M L E M T P H Q G>  
 -----  
 680 \* 690 \* 700 \* 710 \* 720 \*  
 GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC  
 CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG  
 E V Y T C H V E H P S L K S P I>  
 ----- I-Ad  $\beta$ -2 DOMAIN -----  
 730 \* 740 \* 750 \* 760 \* 770 \*  
 ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC  
 TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG  
 T V E W T S G G G G S G G G S>  
 -----><----- 24 AMINO ACID LINKER -----  
 780 \* 790 \* 800 \* 810 \*  
 GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAG GAC ATT  
 CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA  
 G G G G S G G G S S S E D D I>  
 -----><-----  
 820 \* 830 \* 840 \* 850 \* 860 \*  
 GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT  
 CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA  
 E A D H V G F Y G T T V Y Q S P>  
 ----- I-Ad  $\alpha$ -1 DOMAIN -----

FIG.28C

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870	880	890	900	910
*	*	*	*	*
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC				
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG				
G D I G Q Y T H E F D G D E L F>				

920	930	940	950	960
*	*	*	*	*
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT				
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA				
Y V D L D K K K T V W R L P E F>				

970	980	990	1000	1010
*	*	*	*	*
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT				
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA				
G Q L I L F E P Q G G L Q N I A>				

1020	1030	1040	1050
*	*	*	*
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC			
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG			
A E K H N L G I L T K R S N F T>			

----- I-Ad  $\alpha$ -1 DOMAIN -----

1060	1070	1080	1090	1100
*	*	*	*	*
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT				
GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA				
P A T N E A P Q A T V F P K S P>				

-----><----- I-Ad  $\alpha$ -2 DOMAIN -----

1110	1120	1130	1140	1150
*	*	*	*	*
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC				
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG				
V L L G Q P N T L I C F V D N I>				

FIG.28D

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```

      1160      1170      1180      1190      1200
      *        *        *        *        *
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC
AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG
F  P  P  V  I  N  I  T  W  L  R  N  S  K  S  V>
-----

      1210      1220      1230      1240      1250
      *        *        *        *        *
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
T  D  G  V  Y  E  T  S  F  L  V  N  R  D  H  S>
-----

      1260      1270      1280      1290
      *        *        *        *
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
F  H  K  L  S  Y  L  T  F  I  P  S  D  D  D  I>
-----

1300      1310      1320      1330      1340
*        *        *        *        *
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT
Y  D  C  K  V  E  H  W  G  L  E  E  P  V  L  K>
-----
                                I-Ad  $\alpha$ -2 DOMAIN -----

      1350      1360      1370      1380      1390
      *        *        *        *        *
CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAA ACT
GTG ACC CTT GGA CTC TAA GGT CGG GGG TAC AGT CTC GAC TGT CTT TGA
H  W  E  P  E  I  P  A  P  M  S  E  L  T  E  T>
-----
><----- I-Ad  $\alpha$ -TM DOMAIN -----

      1400      1410      1420      1430      1440
      *        *        *        *        *
GTG GTG TGT GCC CTG GGG TTG TCT GTG GGC CTT GTG GGC ATC GTG GTG
CAC CAC ACA CGG GAC CCC AAC AGA CAC CCG GAA CAC CCG TAG CAC CAC
V  V  C  A  L  G  L  S  V  G  L  V  G  I  V  V>
-----

```

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FIG.28E



1450	1460	1470	1480	1490
*	*	*	*	*
GGC ACC ATC TTC ATC ATT CAA GGC CTG CGA TCA GGT GGC ACC TCC AGA				
CCG TGG TAG AAG TAG TAA GTT CCG GAC GCT AGT CCA CCG TGG AGG TCT				
G T I F I I Q G L R S G G T S R>				

---

CAC CCA GGG CCT TTA TGA  
 GTG GGT CCC GGA AAT ACT  
 H P G P L \*>  
 - I-Ad  $\alpha$ -TM DOMAIN ->

FIG.28F

10                      20                      30                      40                      50  
 \*                      \*                      \*                      \*                      \*  
 CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG  
 GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC  
 M A L Q I P S L L L S A A V V>  
 <----- I-Ad  $\beta$  CHAIN LEADER ----->

60                      70                      80                      90  
 \*                      \*                      \*                      \*  
 GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT  
 CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA  
 V L M V L S S P R T L S I S Q A>

100                      110                      120                      130                      140  
 \*                      \*                      \*                      \*                      \*  
 GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA  
 CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT  
 V H A A H A E I N E A G R A S G>  
 ----- OVA 323-339 -----><-----

150                      160                      170                      180                      190  
 \*                      \*                      \*                      \*                      \*  
 GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC  
 CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG  
 G G G S G G G G N S E R H F V V>  
 -- 10 AMINO ACID LINKER --><----- I-Ad  $\beta$ -1 DOMAIN ----->

200                      210                      220                      230                      240  
 \*                      \*                      \*                      \*                      \*  
 CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG  
 GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC  
 Q F K G E C Y Y T N G T Q R I R>

250                      260                      270                      280                      290  
 \*                      \*                      \*                      \*                      \*  
 CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC  
 GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG  
 L V T R Y I Y N R E E Y V R Y D>

FIG.29A

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300                      310                      320                      330  
      \*                      \*                      \*                      \*  
 AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC  
 TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG  
 S    D    V    G    E    Y    R    A    V    T    E    L    G    R    P    D>  
 -----  
 340                      350                      360                      370                      380  
      \*                      \*                      \*                      \*                      \*  
 GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC  
 CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG  
 A    E    Y    W    N    S    Q    P    E    I    L    E    R    T    R    A>  
 -----  
 390                      400                      410                      420                      430  
      \*                      \*                      \*                      \*                      \*  
 GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC  
 CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG  
 E    V    D    T    A    C    R    H    N    Y    E    G    P    E    T    S>  
 -----  
 440                      450                      460                      470                      480  
      \*                      \*                      \*                      \*                      \*  
 ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC  
 TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG  
 T    S    L    R    R    L    E    Q    P    N    V    A    I    S    L    S>  
 --- I-Ad  $\beta$ -1 DOMAIN --<----- I-Ad  $\beta$ -2 DOMAIN -----  
 -----  
 490                      500                      510                      520                      530  
      \*                      \*                      \*                      \*                      \*  
 AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA  
 TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT  
 R    T    E    A    L    N    H    H    N    T    L    V    C    S    V    T>  
 -----  
 540                      550                      560                      570  
      \*                      \*                      \*                      \*  
 GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG  
 CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC  
 D    F    Y    P    A    K    I    K    V    R    W    F    R    N    G    Q>  
 -----

FIG.29B

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580															
*															
GAG	GAG	ACA	GTG	GGG	GTC	TCA	TCC	ACA	CAG	CTT	ATT	AGG	AAT	GGG	GAC
CTC	CTC	TGT	CAC	CCC	CAG	AGT	AGG	TGT	GTC	GAA	TAA	TCC	TTA	CCC	CTG
E	E	T	V	G	V	S	S	T	Q	L	I	R	N	G	D>
-----															
630															
*															
TGG	ACC	TTC	CAG	GTG	CTG	GTC	ATG	CTG	GAG	ATG	ACC	CCT	CAT	CAG	GGA
ACC	TGG	AAG	GTC	CAG	GAC	CAG	TAC	GAC	CTC	TAC	TGG	GGA	GTA	GTC	CCT
W	T	F	Q	V	L	V	M	L	E	M	T	P	H	Q	G>
-----															
680															
*															
GAG	GTC	TAC	ACC	TGC	CAT	GTG	GAG	CAT	CCC	AGC	CTG	AAG	AGC	CCC	ATC
CTC	CAG	ATG	TGG	ACG	GTA	CAC	CTC	GTA	GGG	TCG	GAC	TTC	TCG	GGG	TAG
E	V	Y	T	C	H	V	E	H	P	S	L	K	S	P	I>
-----															
I-Ad $\beta$ -2 DOMAIN															
730															
*															
ACT	GTG	GAG	TGG	ACT	AGT	GGT	GGC	GGT	GGC	AGC	GGC	GGT	GGT	GGT	TCC
TGA	CAC	CTC	ACC	TGA	TCA	CCA	CCG	CCA	CCG	TCG	CCG	CCA	CCA	CCA	AGG
T	V	E	W	T	S	G	G	G	G	S	G	G	G	G	S>
-----															
><----- 24 AMINO ACID LINKER -----															
780															
*															
GGT	GGC	GGC	GGT	TCT	GGC	GGT	GGC	GGT	TCC	TCG	AGT	GAA	GAC	GAC	ATT
CCA	CCG	CCG	CCA	AGA	CCG	CCA	CCG	CCA	AGG	AGC	TCA	CTT	CTG	CTG	TAA
G	G	G	G	S	G	G	G	G	S	S	S	E	D	D	I>
-----															
><-----															
820															
*															
GAG	GCC	GAC	CAC	GTA	GGC	TTC	TAT	GGT	ACA	ACT	GTT	TAT	CAG	TCT	CCT
CTC	CGG	CTG	GTG	CAT	CCG	AAG	ATA	CCA	TGT	TGA	CAA	ATA	GTC	AGA	GGA
E	A	D	H	V	G	F	Y	G	T	T	V	Y	Q	S	P>
-----															
I-Ad $\alpha$ -1 DOMAIN															

FIG. 29C

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870 *	880 *	890 *	900 *	910 *
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC				
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG				
G D I G Q Y T H E F D G D E L F>				
-----				
920 *	930 *	940 *	950 *	960 *
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT				
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA				
Y V D L D K K K T V W R L P E F>				
-----				
970 *	980 *	990 *	1000 *	1010 *
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT				
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA GCT GAC GTT TTG TAT CGA				
G Q L I L F E P Q G G L Q N I A>				
-----				
1020 *	1030 *	1040 *	1050 *	
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC				
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG				
A E K H N L G I L T K R S N F T>				
----- I-Ad $\alpha$ -1 DOMAIN -----				
-----				
1060 *	1070 *	1080 *	1090 *	1100 *
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT				
GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA				
P A T N E A P Q A T V F P K S P>				
-----><----- I-Ad $\alpha$ -2 DOMAIN -----				
-----				
1110 *	1120 *	1130 *	1140 *	1150 *
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC				
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG				
V L L G Q P N T L I C F V D N I>				
-----				

FIG.29D

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FIG. 29E

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC TCA GCT GCT GTG GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT GTT CAC  
M A L Q I P S L L L S A A V V V L M V L S S P R T L S I S Q A V H  
Kozak  
consensus  
IA<sup>d</sup> β chain signal peptide  
GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG // AGC CCC ATC ACT GTG GAG TGG  
A A H A E I N E A G R A S G G G G S G G G G N S E R // S P I T V E W  
--- OVA 323-339 peptide --- Peptide linker --- IA<sup>d</sup> β1-β2 domains --- aa189  
ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT TCC GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT // CCA GGC CCT TTA TGA  
T S G G G S G G G S G G G S G G G S S S E D D I // P G P L .  
Single chain linker --- aa1  
IA<sup>d</sup> α chain --- Stop

FIG. 30

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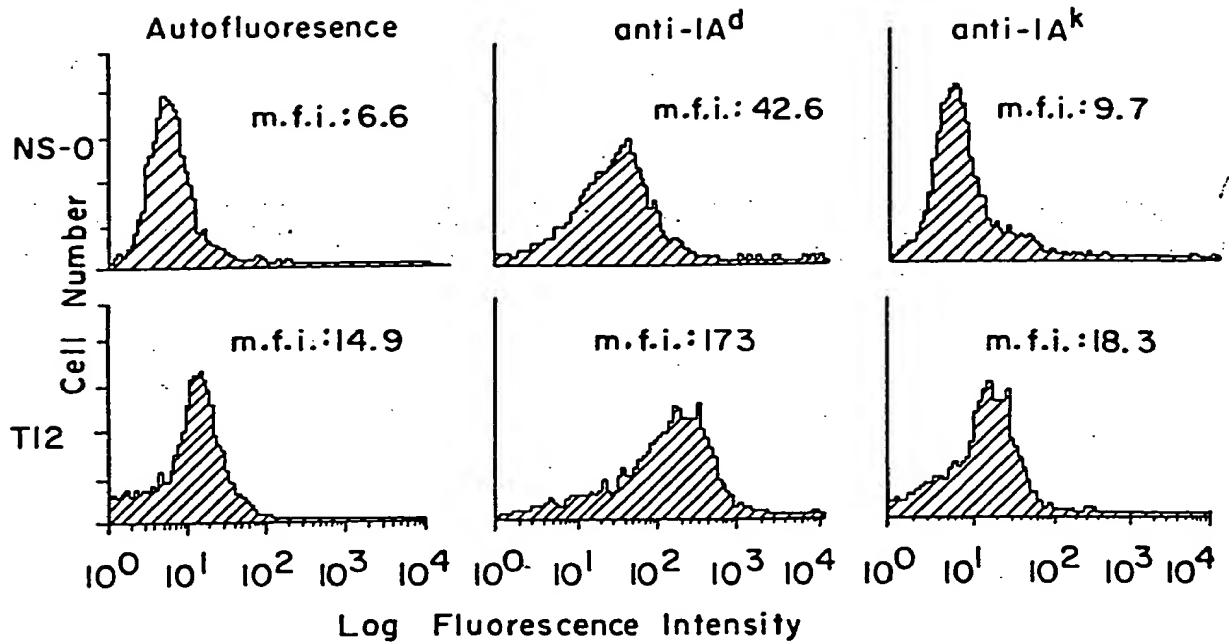


FIG. 3IA

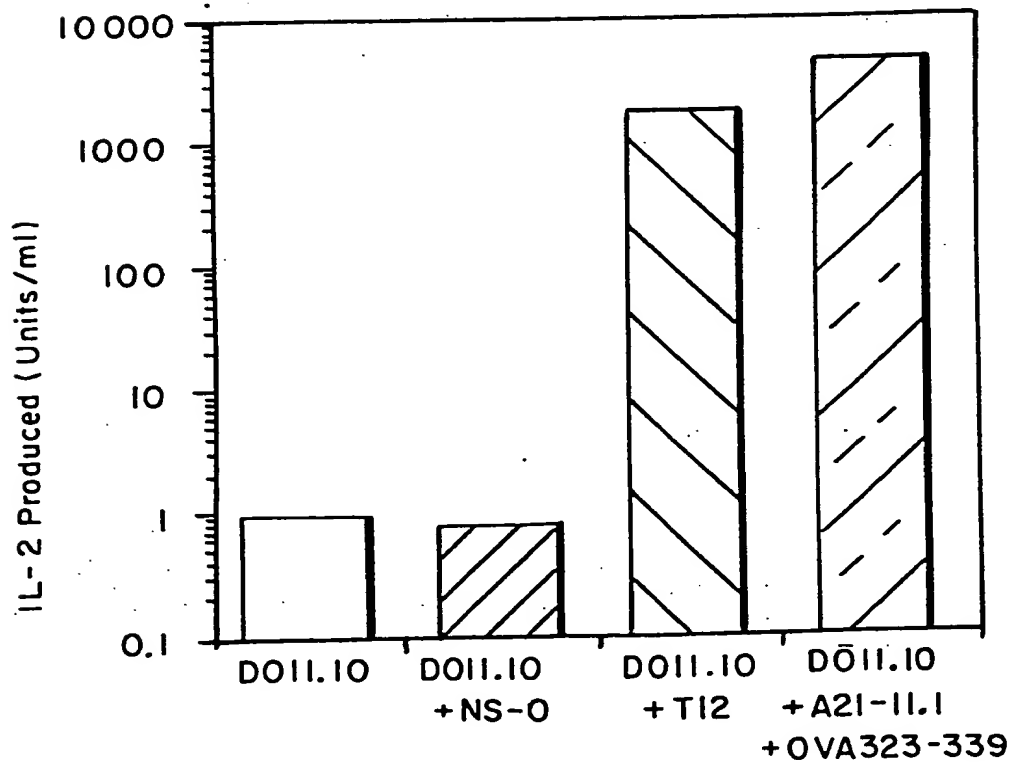


FIG. 3IB



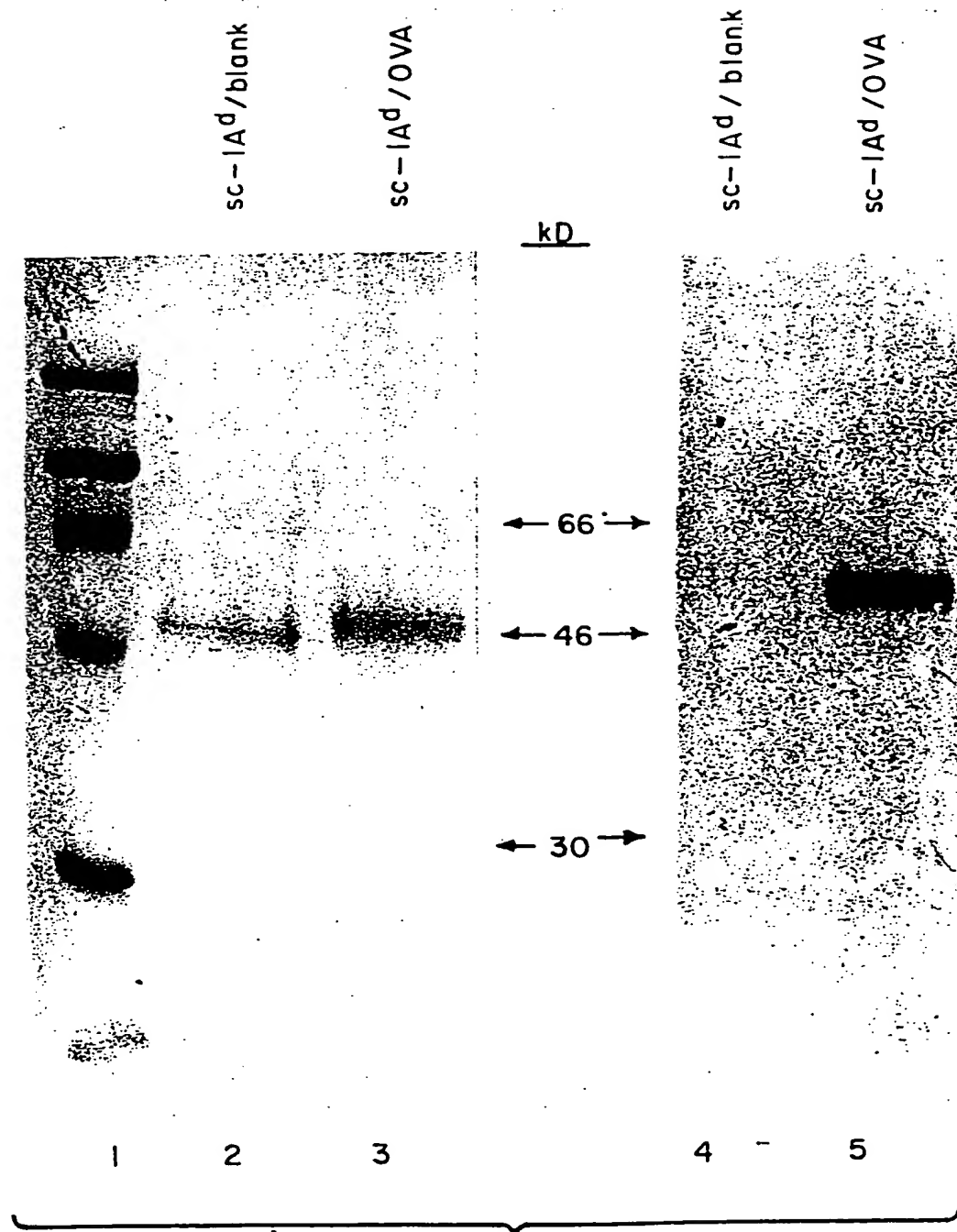


FIG.32

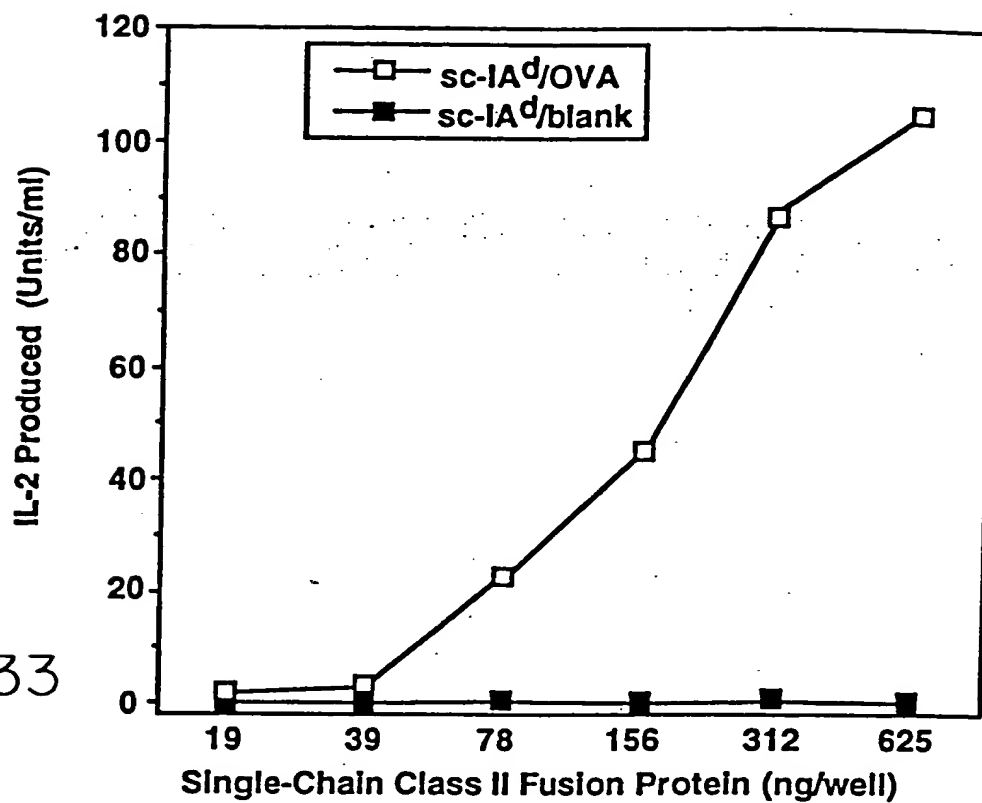


FIG.33

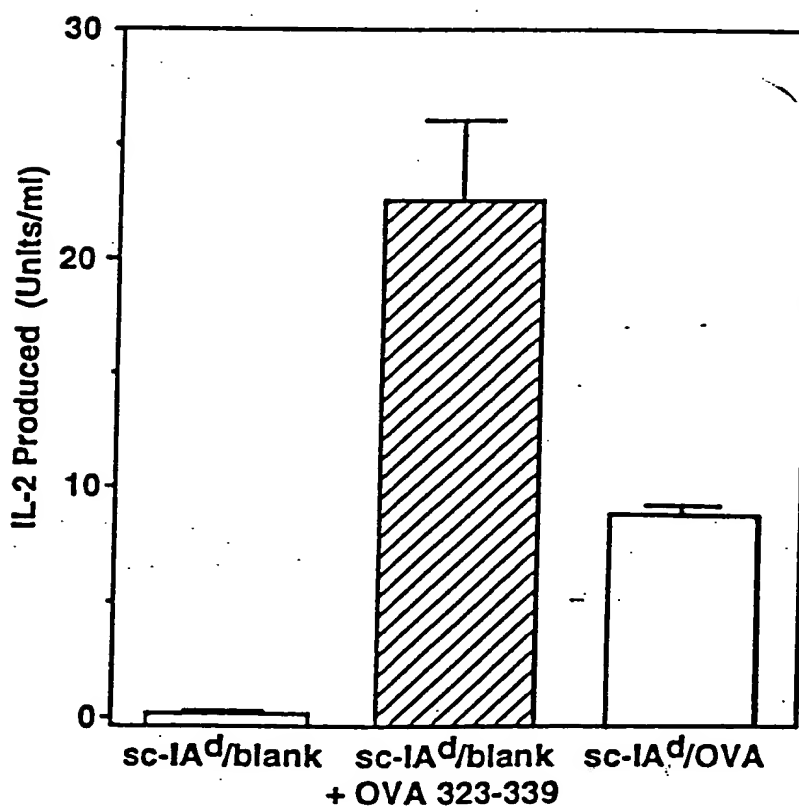


FIG.34C

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FIG.34A

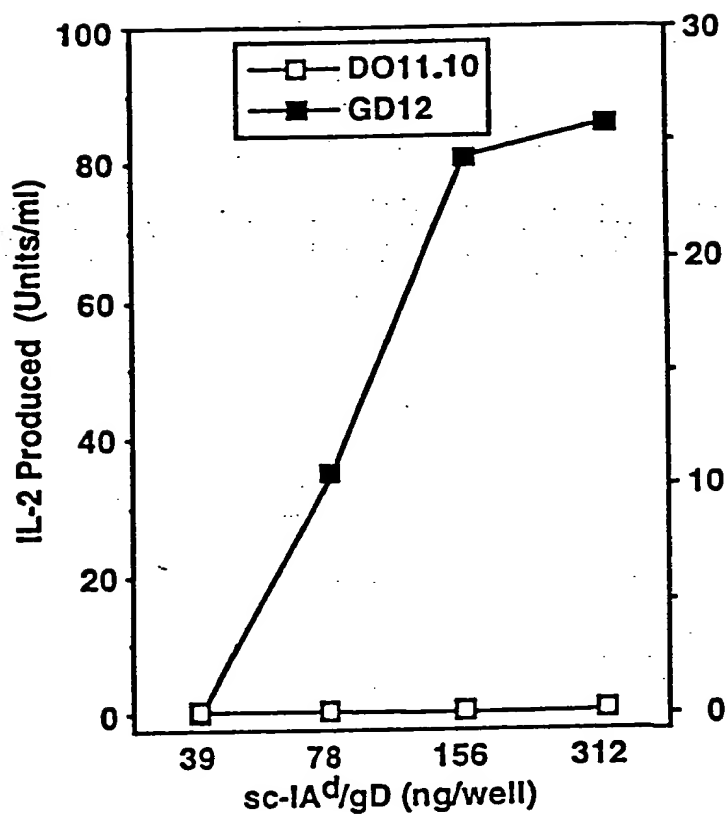
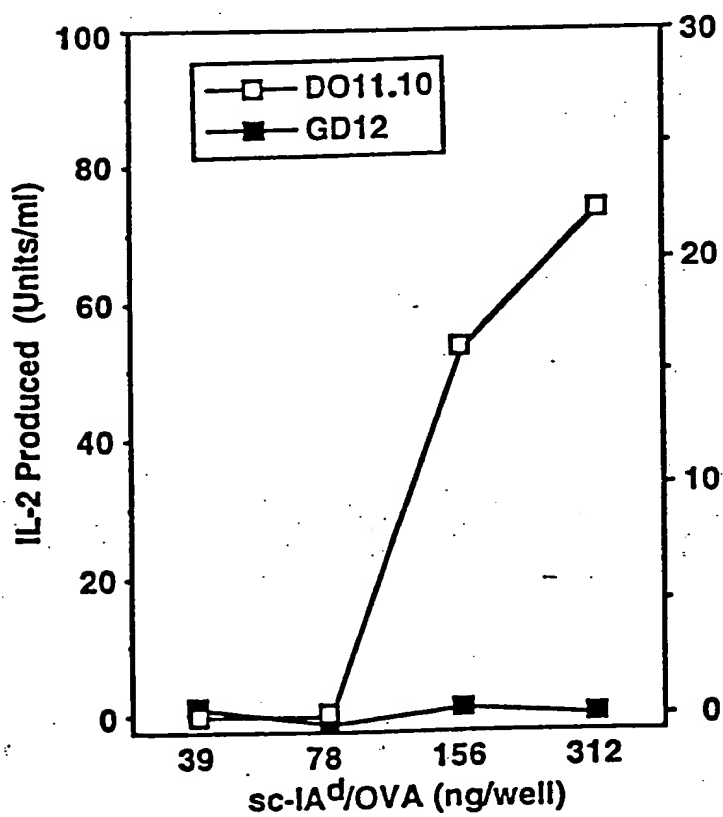


FIG.34B



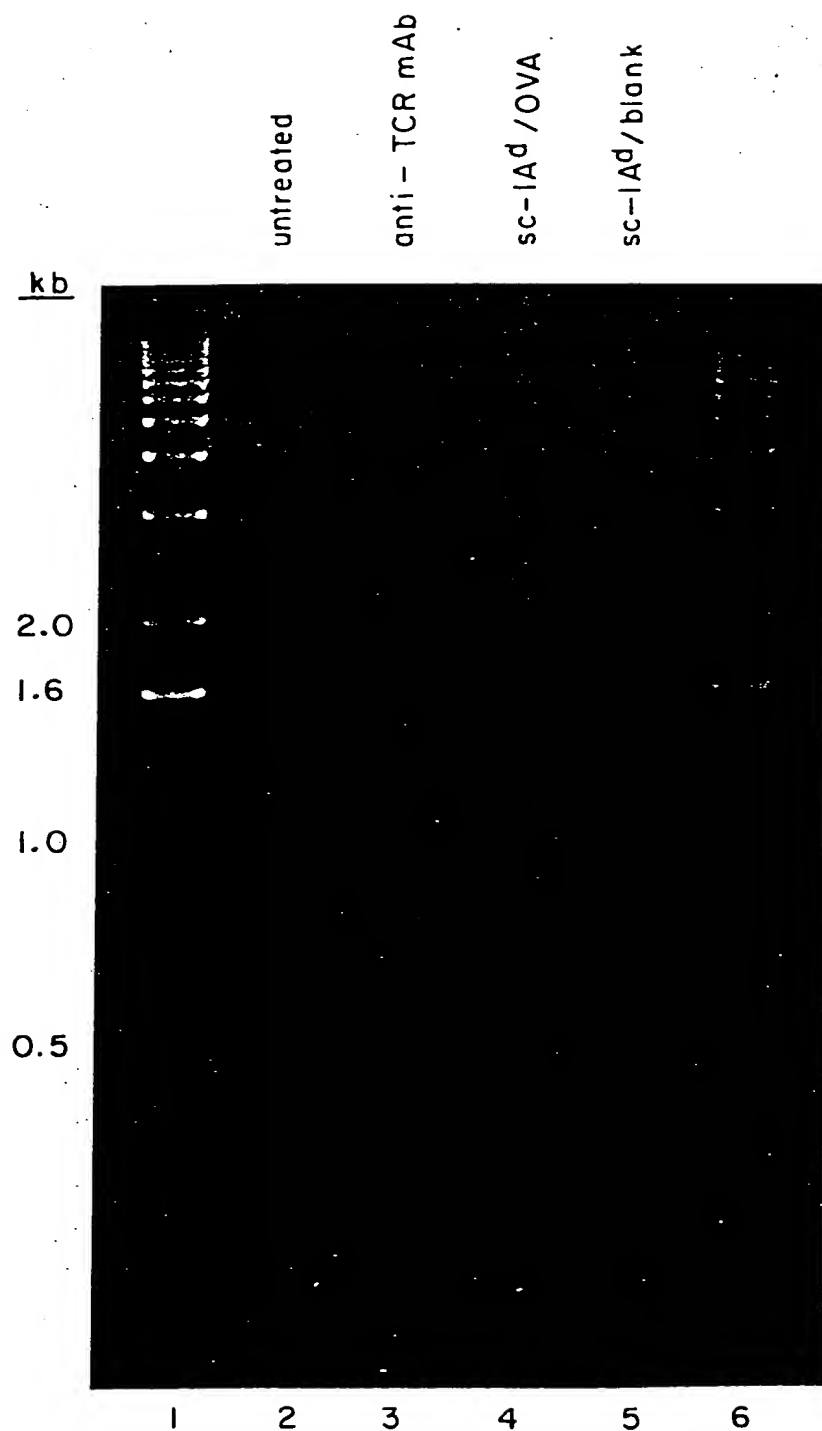


FIG. 35

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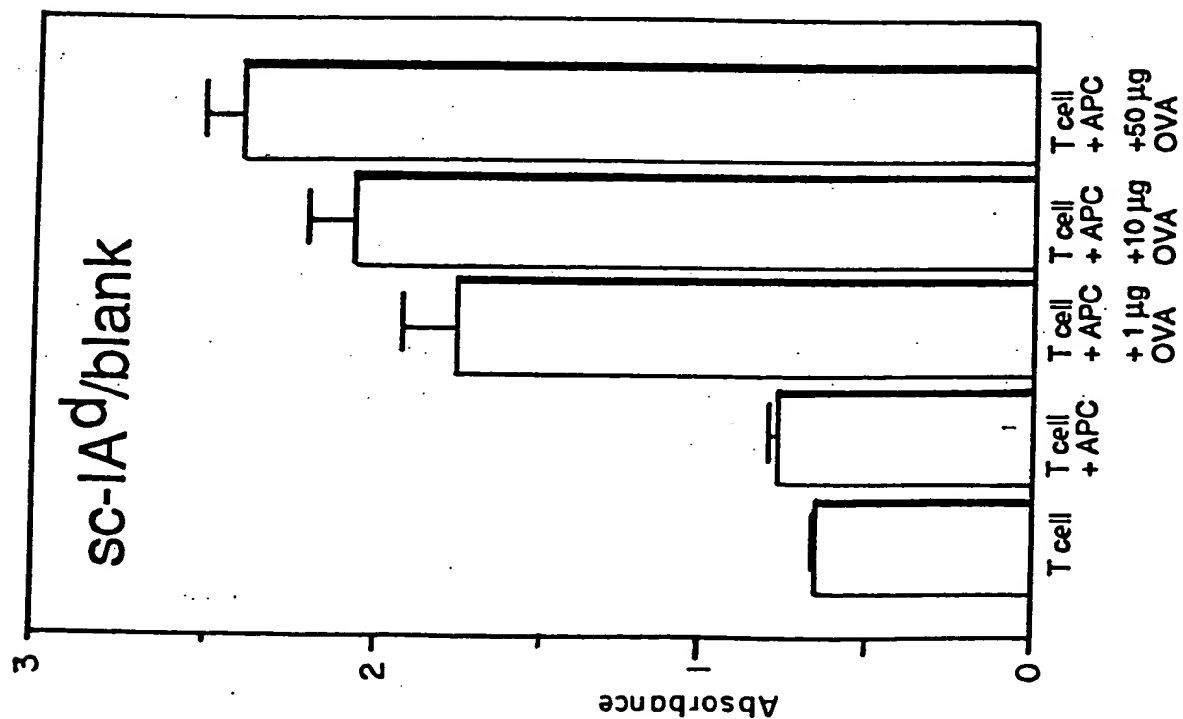


FIG. 36A

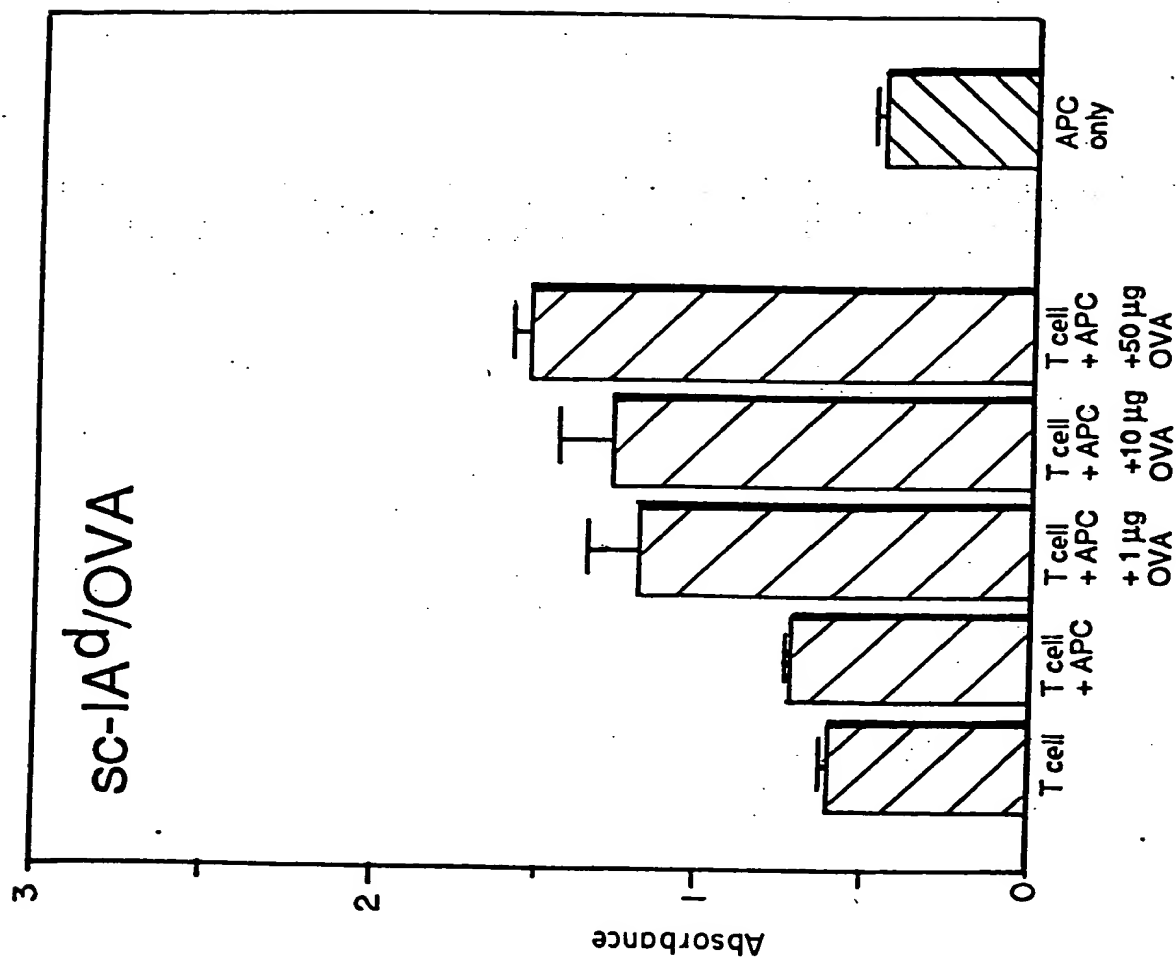


FIG. 36B